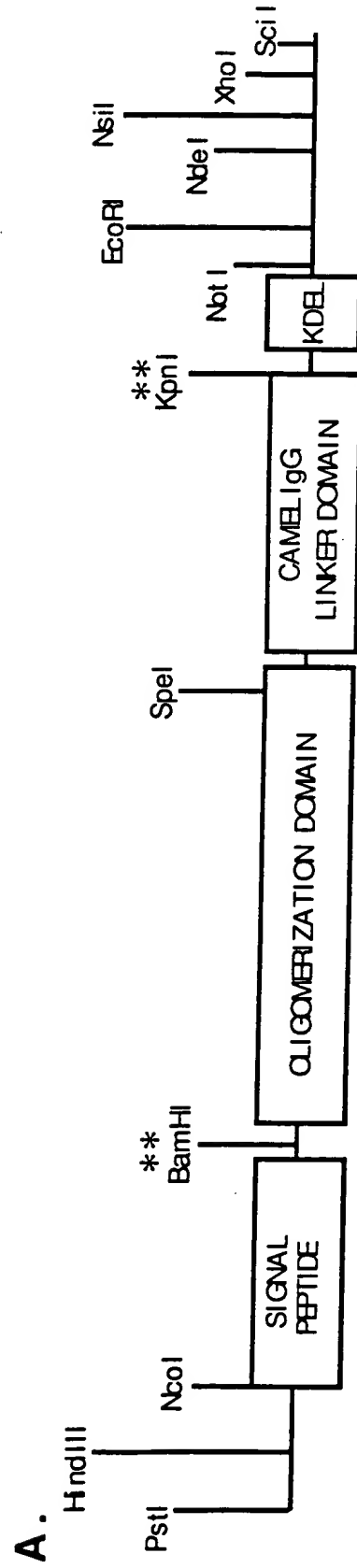


Figure 1: Schematic Representation of KDEL Receptor-Inhibitor Protein and Its Amino Acid Sequences
(Rat COMP oligomerization domain)



B.

Signal cleavage site

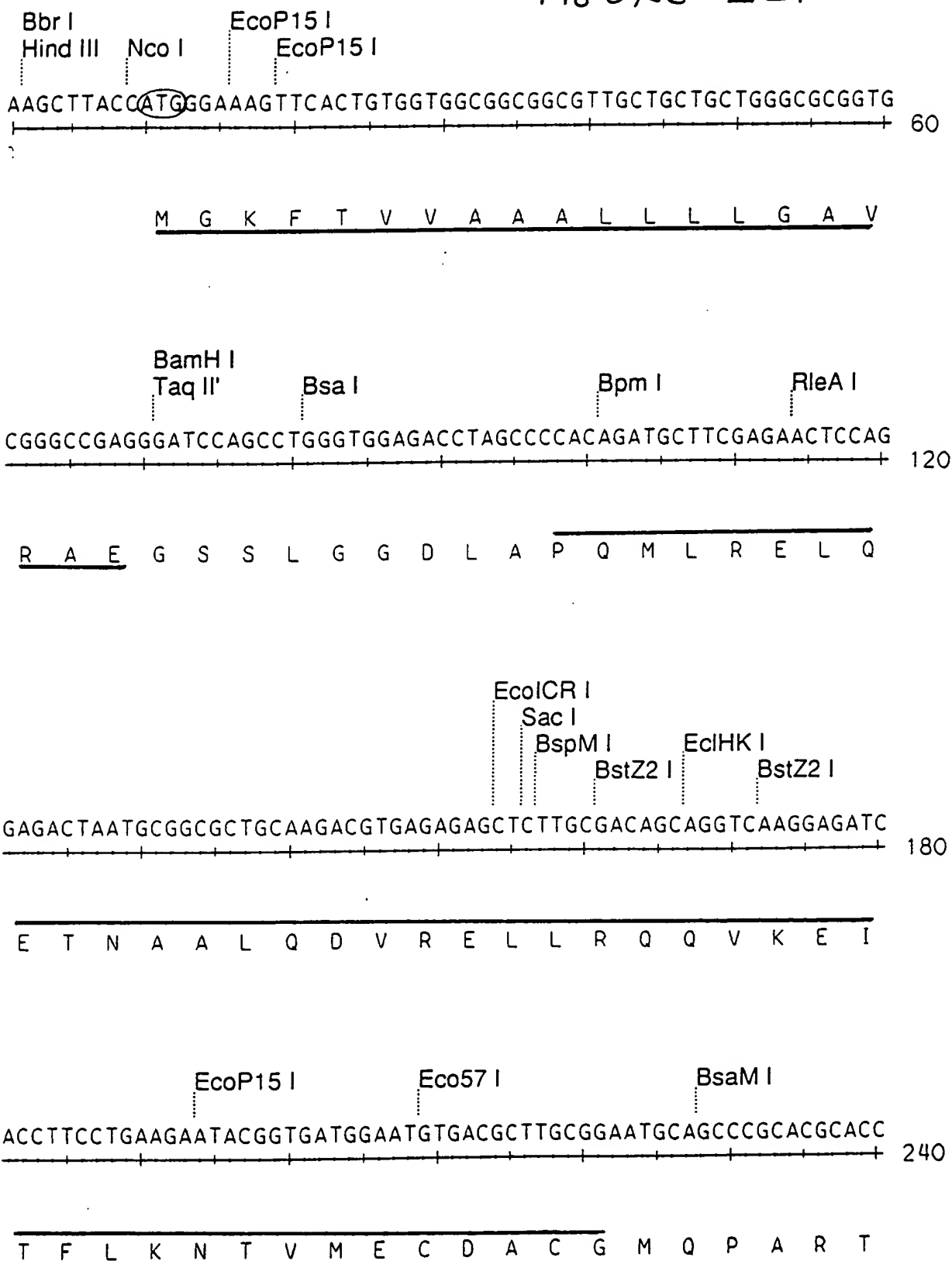
MGKFTVVAALLLLGAVRAE-GSS -

LGGDLA-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQPKPQPQPQPKPQPKPEPE-GTGSSE-KDEL

3145 (sheet 2 of 5)

FIGURE 1C.



3. f8 (sheet 3 of 2)

Spe I

CCCGGTACTAGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGCGAGCCGAAA 300

P G T S P Q P Q P K P Q P Q P Q P Q P K

Acc65 I

Kpn I

Eco52 I

CCGCAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAGGCG 360

P Q P K P E P E G T G S S E K D E L

FIGURE 1D.

Nde I

Ppu10 I

BfrB I

Nsi I

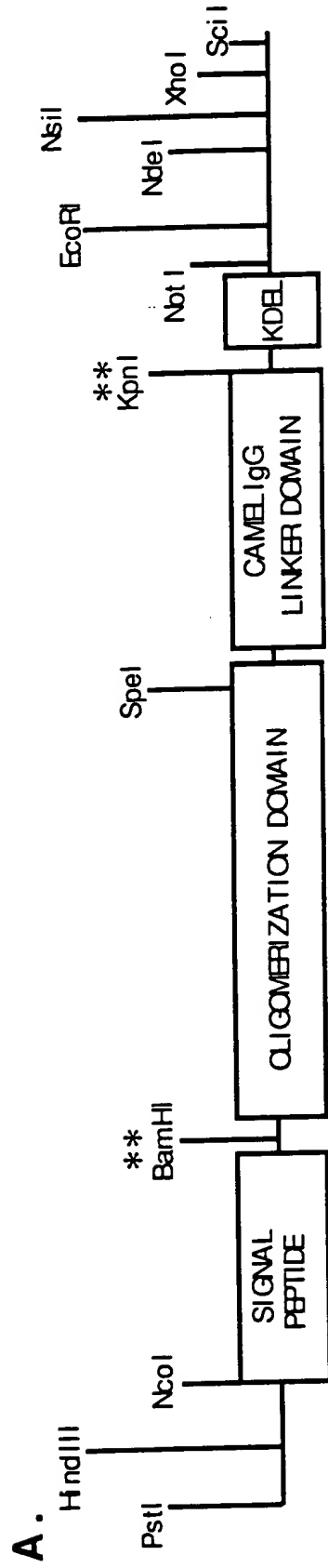
Xho I

Sci I

EcoR I

GCCGCAGAATTCCATATGCATCTCGAG 387

Figure 2: Schematic Representation of KDEL Receptor-Inhibitor Protein and Its Amino Acid Sequences
(Rat COMP oligomerization domain)



B.

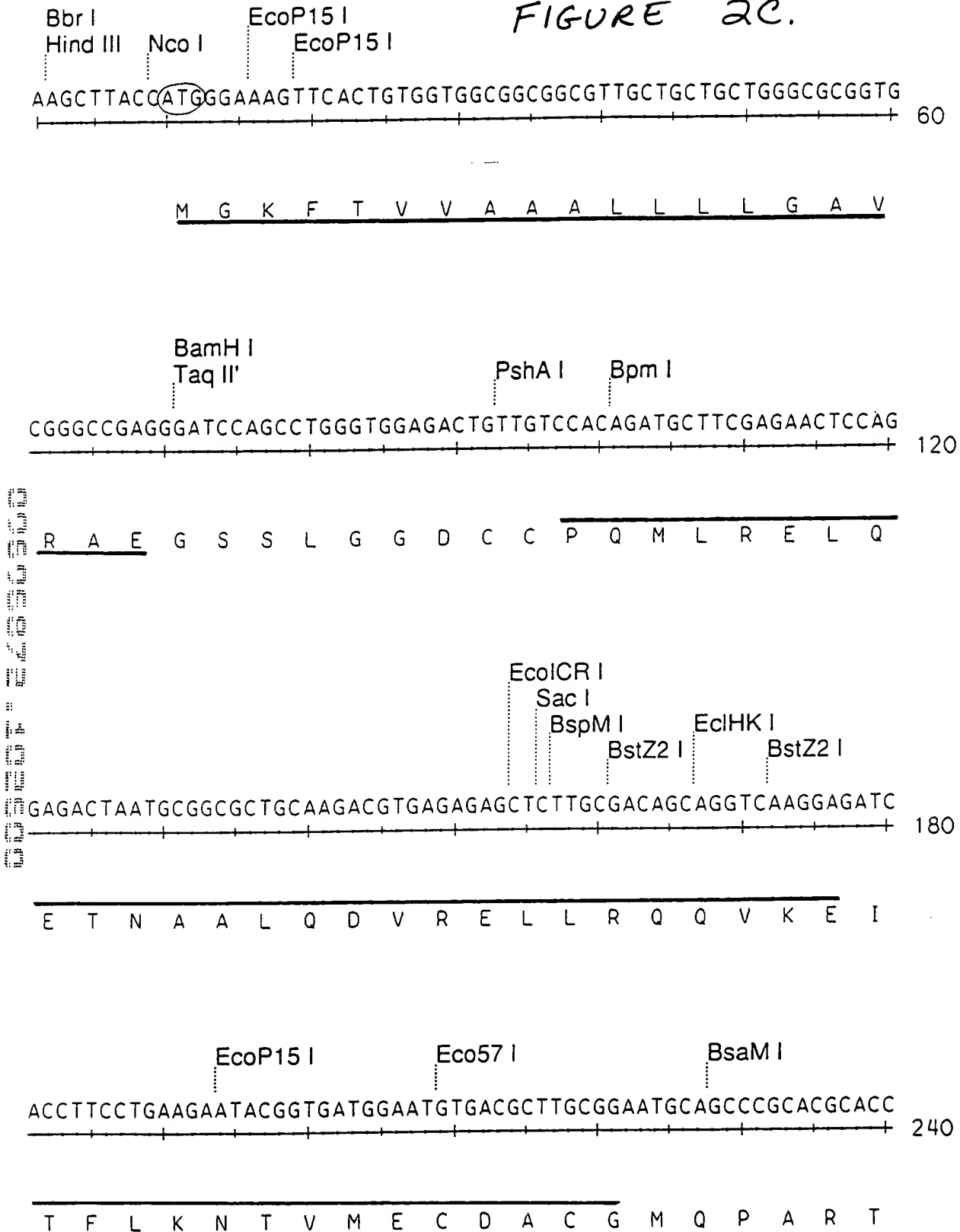
Signal cleavage site

MGKFTVVAAALLLLGAVRAE-GSS -

LGGDCC-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQKPQPQPQPQPQPQPPEPE-GTGSSE-KDEL

FIGURE 2C.



318 (sheet 6 of 30)

Spe I

CCCGGTACTAGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAA 300

P G T S P Q P Q P K P Q P Q P Q P K

Acc65 I

Kpn I

Eco52 I

CCGCAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAG GCG 360

P Q P K P E P E G T G S S E K D E L .

FIGURE 2D.

Nde I

Ppu10 I

BfrB I

Nsi I

Xho I

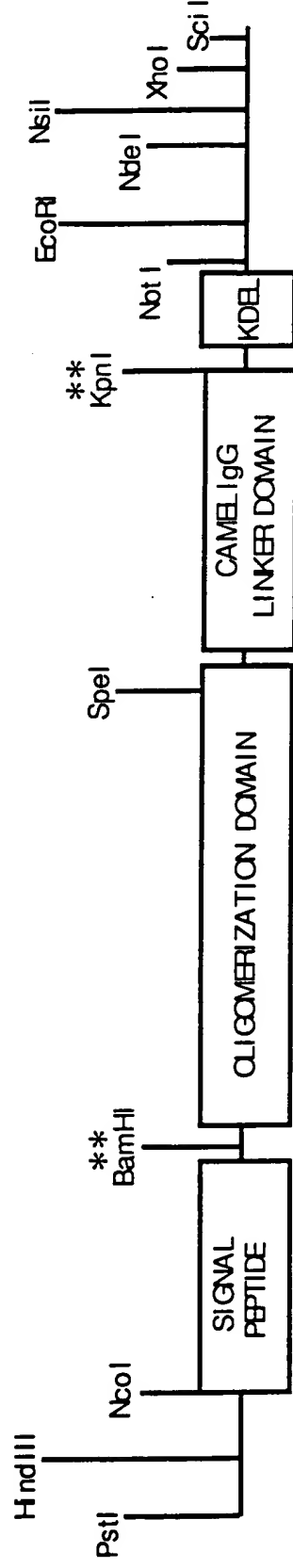
Sci I

EcoR I

GCCGCAGAATTCCATATGCATCTCGAG 387

Figure 3: MOUSE TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site

MGKFTVVAALLLLGAVRAE-GSS -

LGGDCC-KALVTQLTFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPKPQPQPQPQPQPQPPEPE-GTGSSE-KDEL

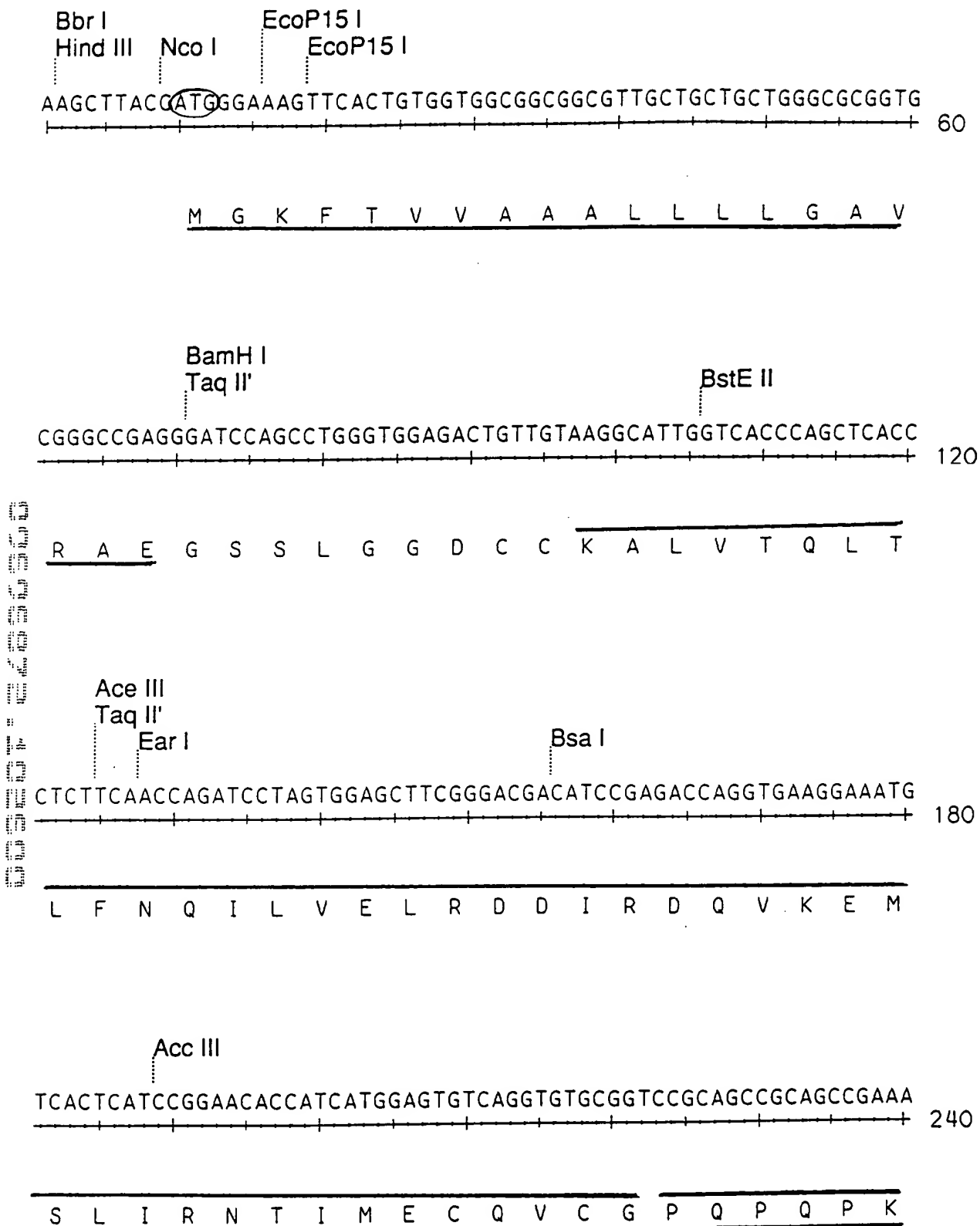


FIGURE 3C.

3148 (sheet 9 of 30)

CCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGAAGGTACC 300

Acc65 I
Kpn I

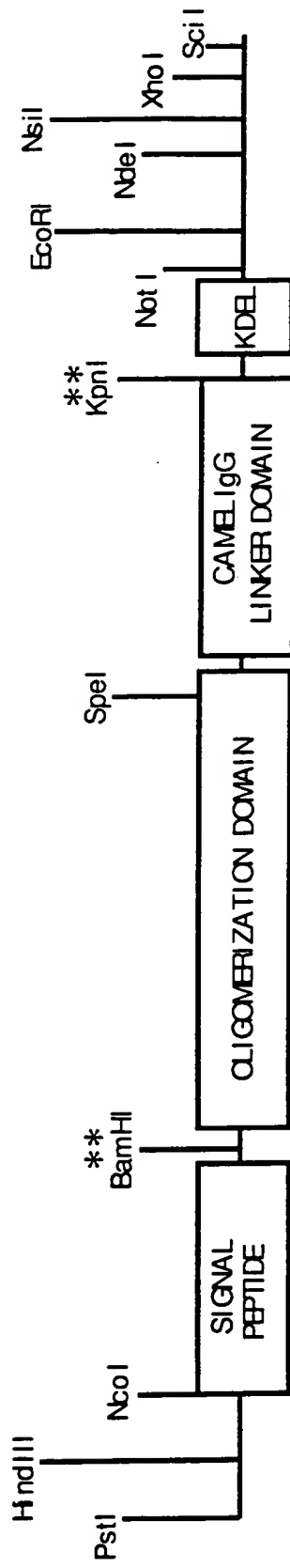
P Q P Q P Q P Q P K P Q P K P E P E G T

The diagram shows a 357 bp DNA fragment with the following restriction sites (from left to right): Eco52 I, EcoR I, Nde I, Ppu10 I, BfrB I, Nsi I, Xho I, and Sci I. The DNA sequence is GGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAAATTCATATGCATCTCGAG. The TAG codon is highlighted with a box. Below the DNA sequence, the amino acid sequence G S S E K D E L . is shown.

FIGURE 3D.

Figure 4: MOUSE TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site



MGKFTVAAALLLLGAVRAE-GSS -

LGGDCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

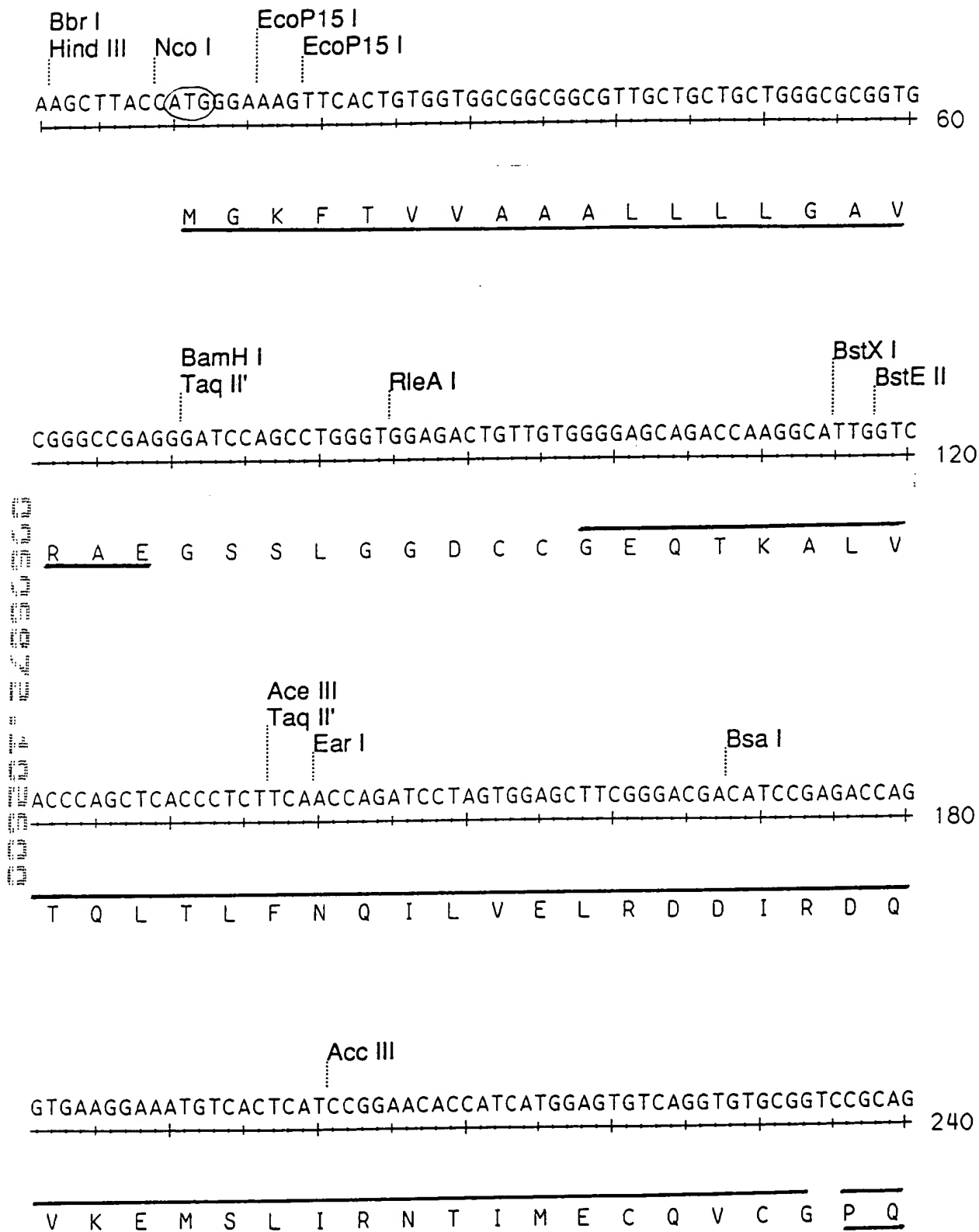


FIGURE 4C.

31.88 (sheet 12 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAG GCGGCCGCAGAATTCCATATG 360

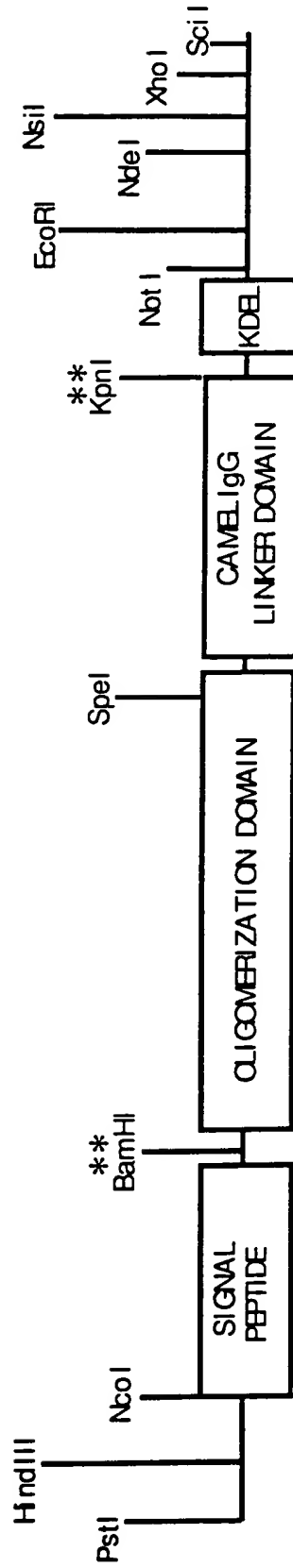
P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 4D.

Figure 5: XENOPUS TSP4 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site

MGKFTVVAALLLGAVRAE-GSS-

LGGDCC-GDVSRQLIGQITQMNQMLGELRDVMRQQVKETMFLRNTIAECQACG-

PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

488 (sheet 1 of 30)

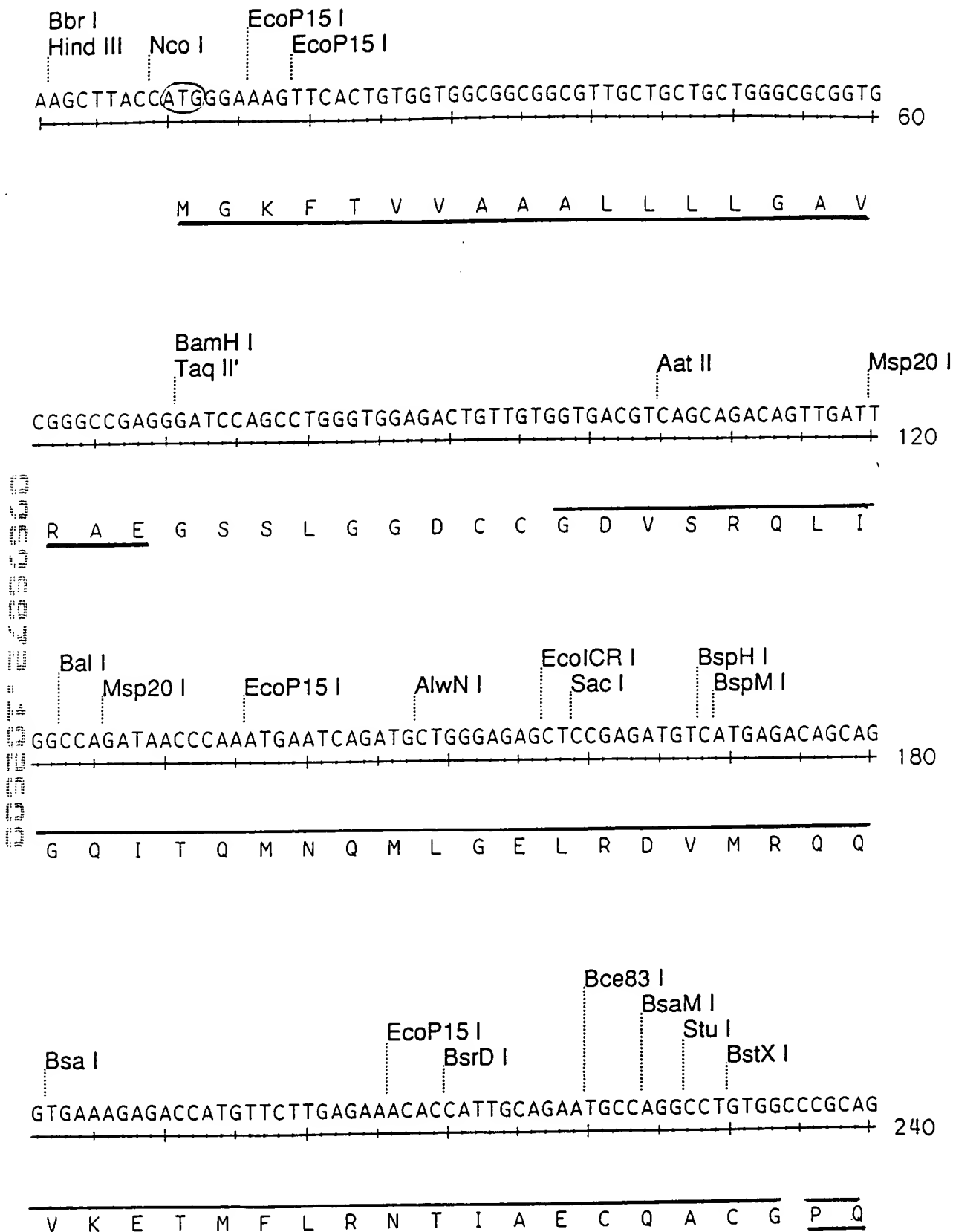


FIGURE 5C

31408 (sheet 15 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

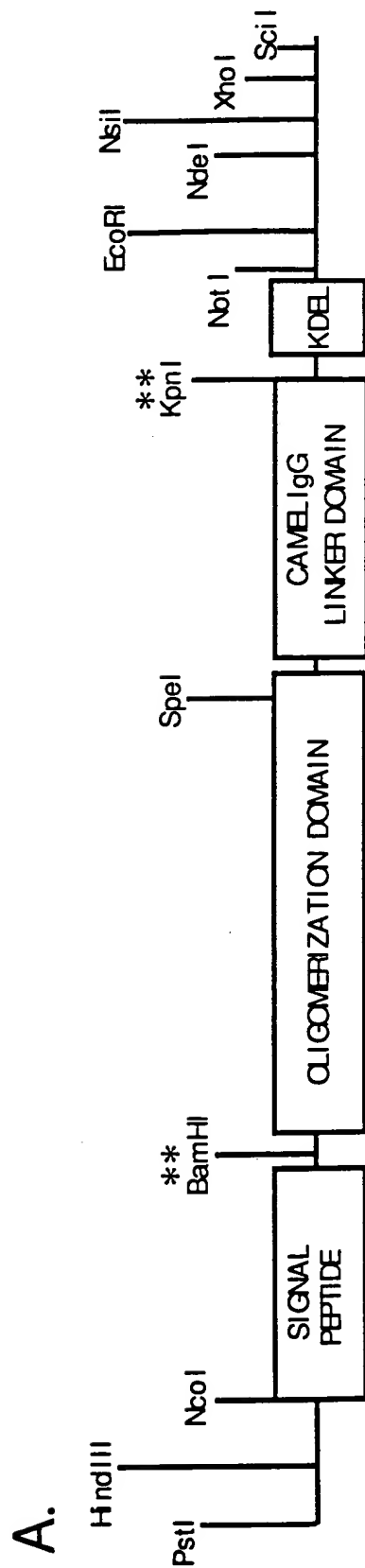
Acc65 I
 Kpn I
 Eco52 I
 EcoR I
 Nde I
 Ppu10 I
 BfrB I
 CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360
 ATAC

P E G T G S S E K D E L .

FIGURE 5D.

Nsi I
 Xho I
 Sci I
 CATCTCGAG 369

Figure 6: HUMAN COMP OLIGOMERIZATION DOMAIN
KDEL RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACG-

PQPQPKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

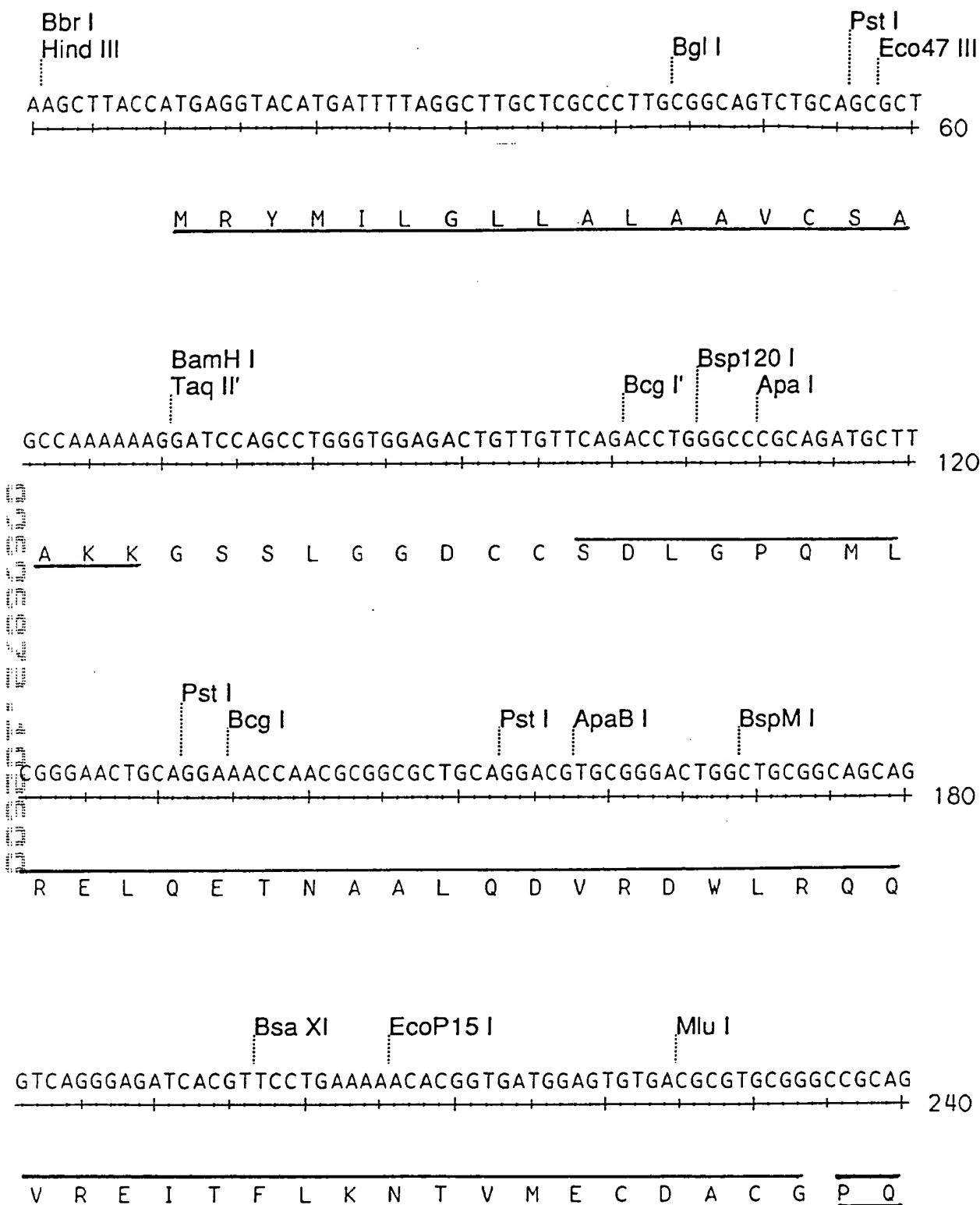


FIGURE 6C.

3188 (sheet 18 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

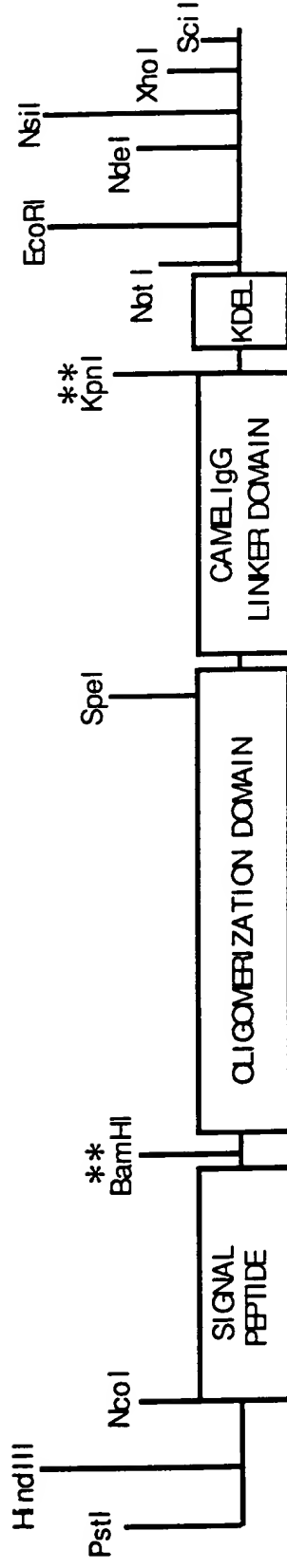
P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 6D.

Figure 7: HUMAN PLB OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site

MRYMILGLLALAAVCSAAKK-GSS-

LGGDCC-QKLQNLFINFCLILICLLICIIVMLL-

POQPKPOQPOQPKPOKPEPE-GTGSSE-KDEL

- Residues critical for pentamer formation

388 (sheet 2 of 30)

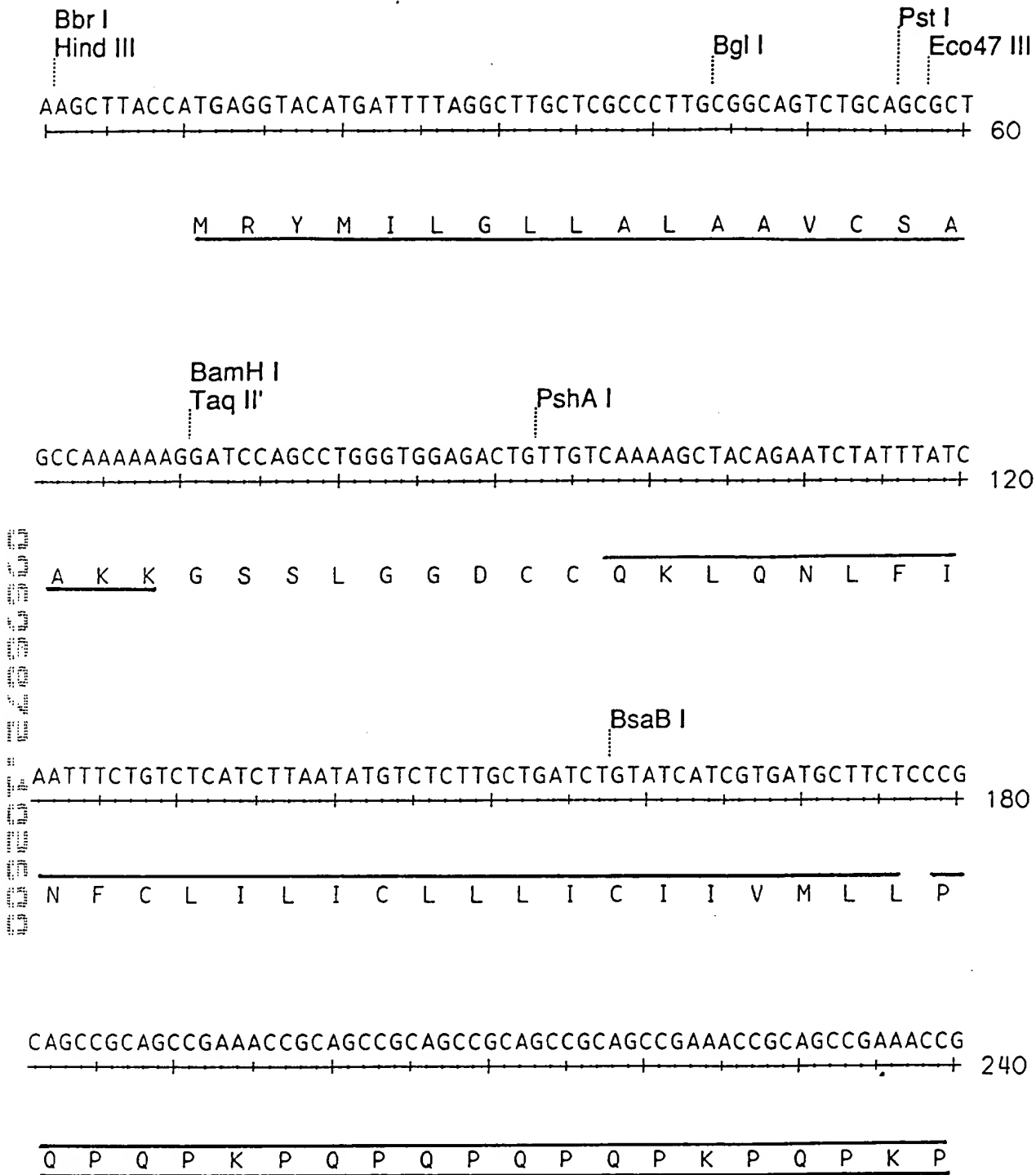


FIGURE 7C.

1488 (sheet 2 of 30)

Acc65 I Kpn I Eco52 I EcoR I Nde I

GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT 300

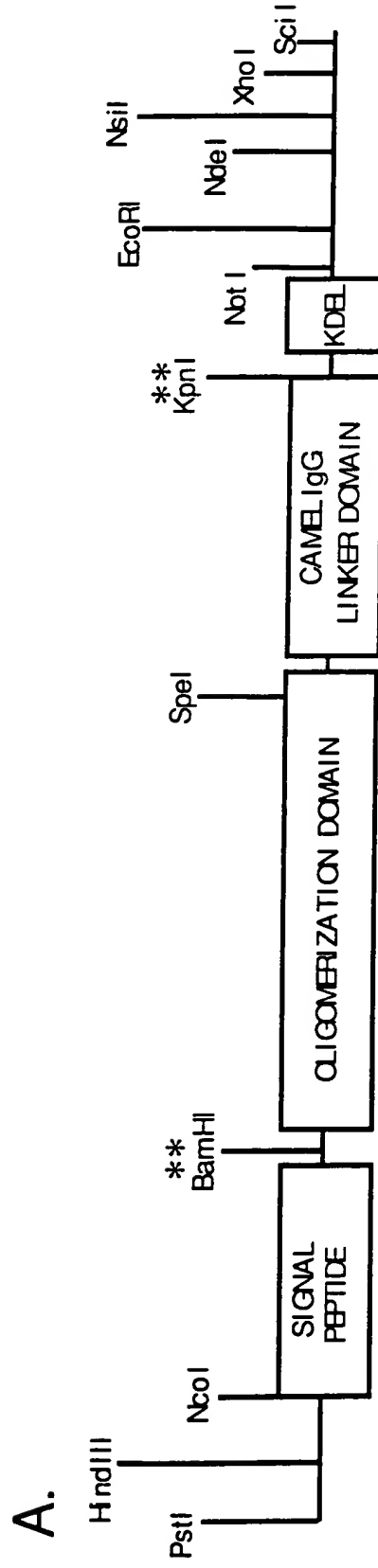
E P E G T G S S E K D E L .

Ppu10 I
BfrB I
Nsi I
Xho I
Sci I

ATGCATCTCGAG 312

FIGURE 7D.

Figure 8: HUMAN TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQPKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

1488 (sheet 2 of 30)

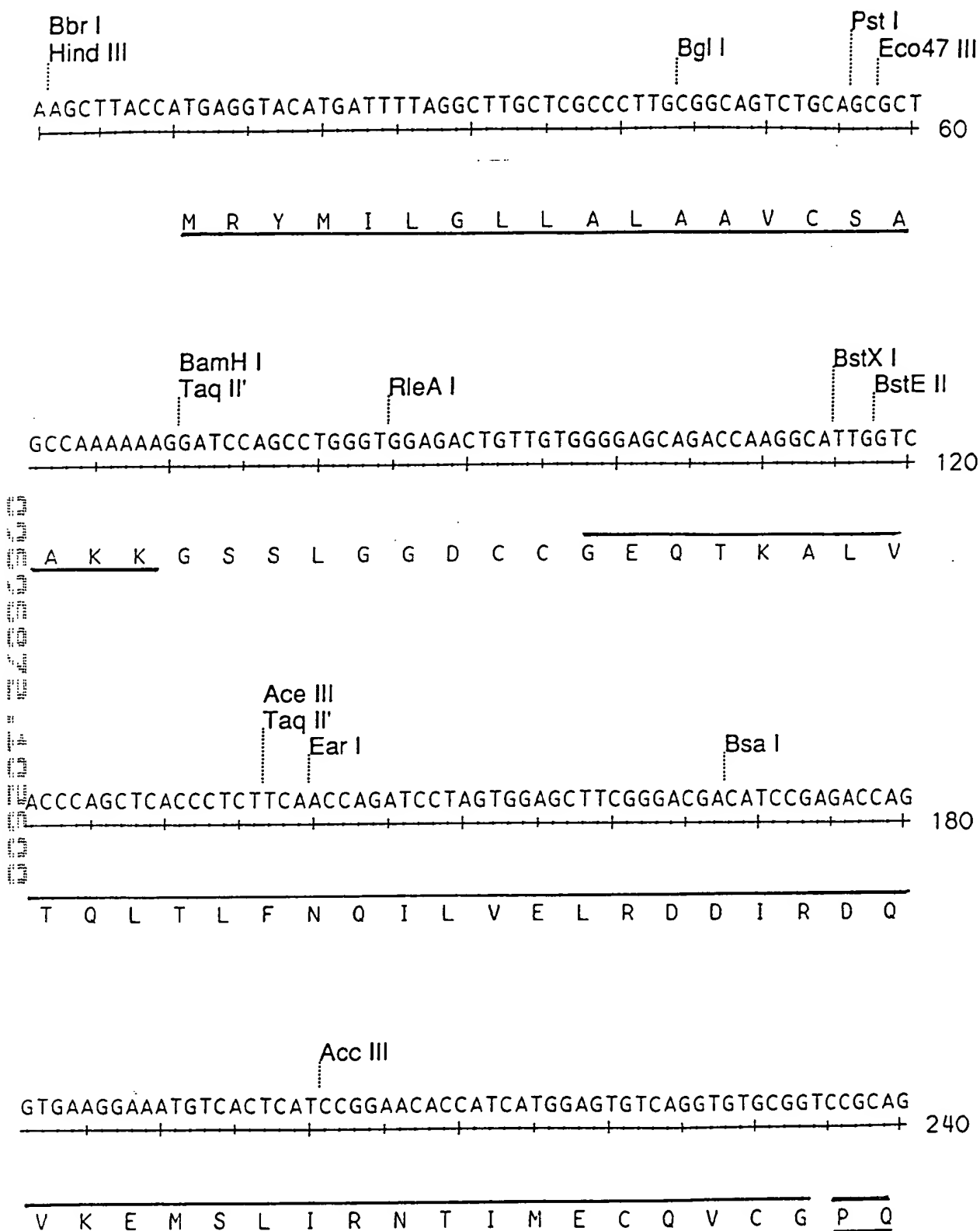


FIGURE 8C.

3148 (sheet 24 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

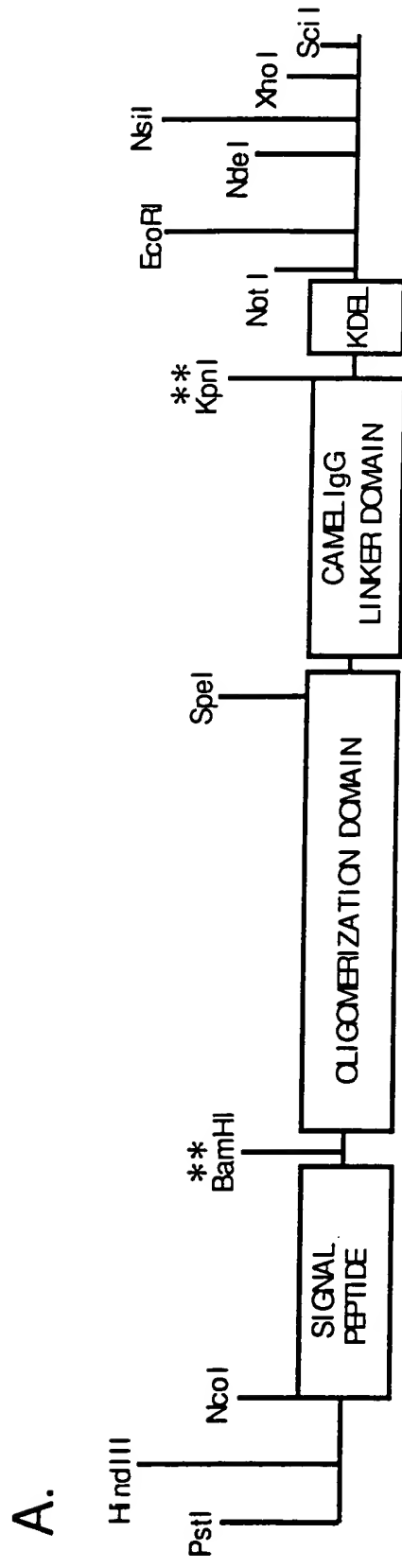
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .


Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 8D.

Figure 9: HUMAN TSP4 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-GDFNRQFLGQMTQLNQLLGEVKDLLRQQVKETSFRLRNTIAECQACG-

PQPQKPQPQPQPQPKPQPKPEPE-GTGSSE-KDEL

1488 (sheet 2 of 30)

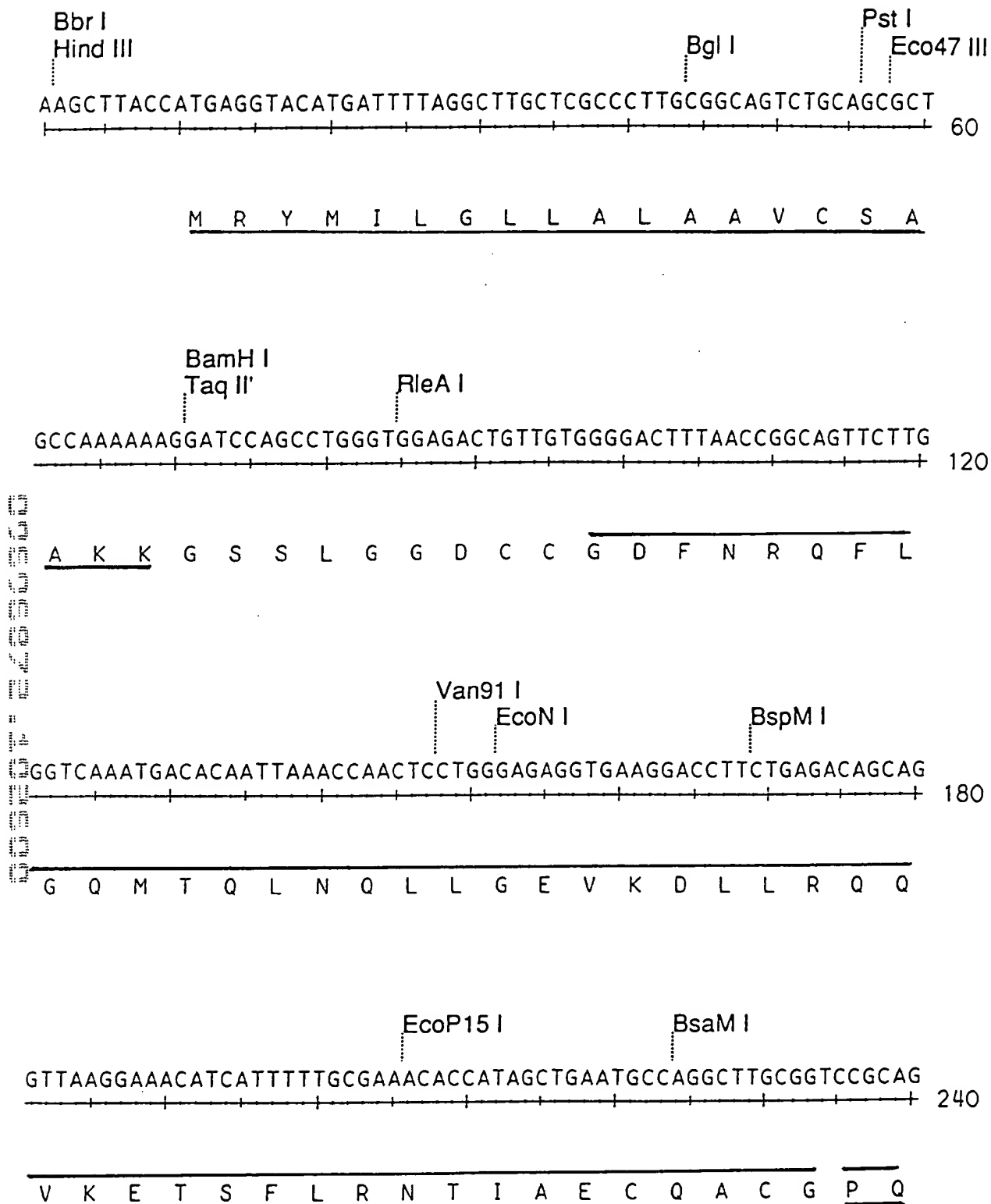


FIGURE 9C.

3488 (sheet 27 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

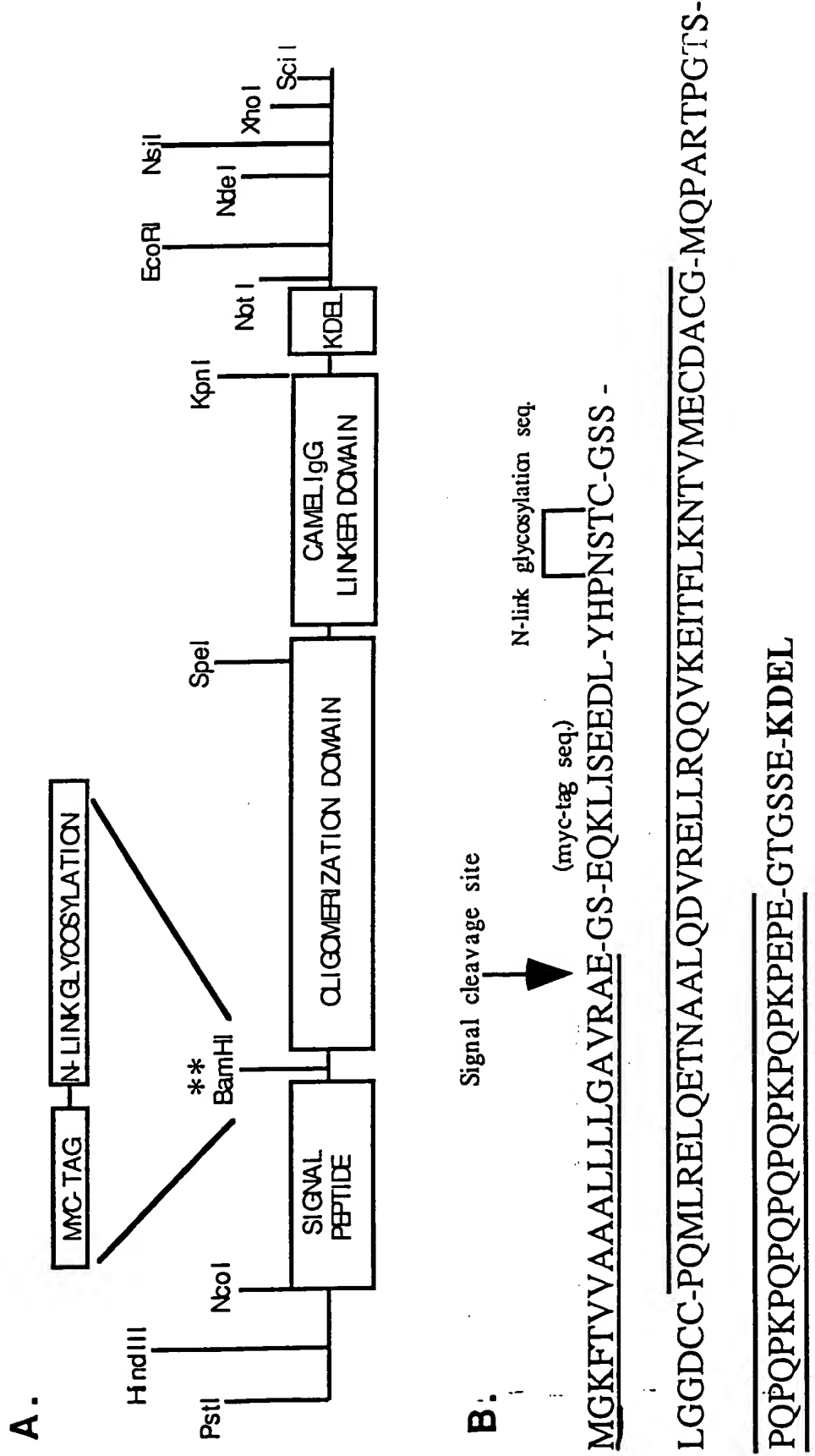
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 9D.

Figure 10: KDEL Inhibitor Protein with myc-tag and a N-linked Glycosylation Sequence



34 is (sheet 29 ~ 30)

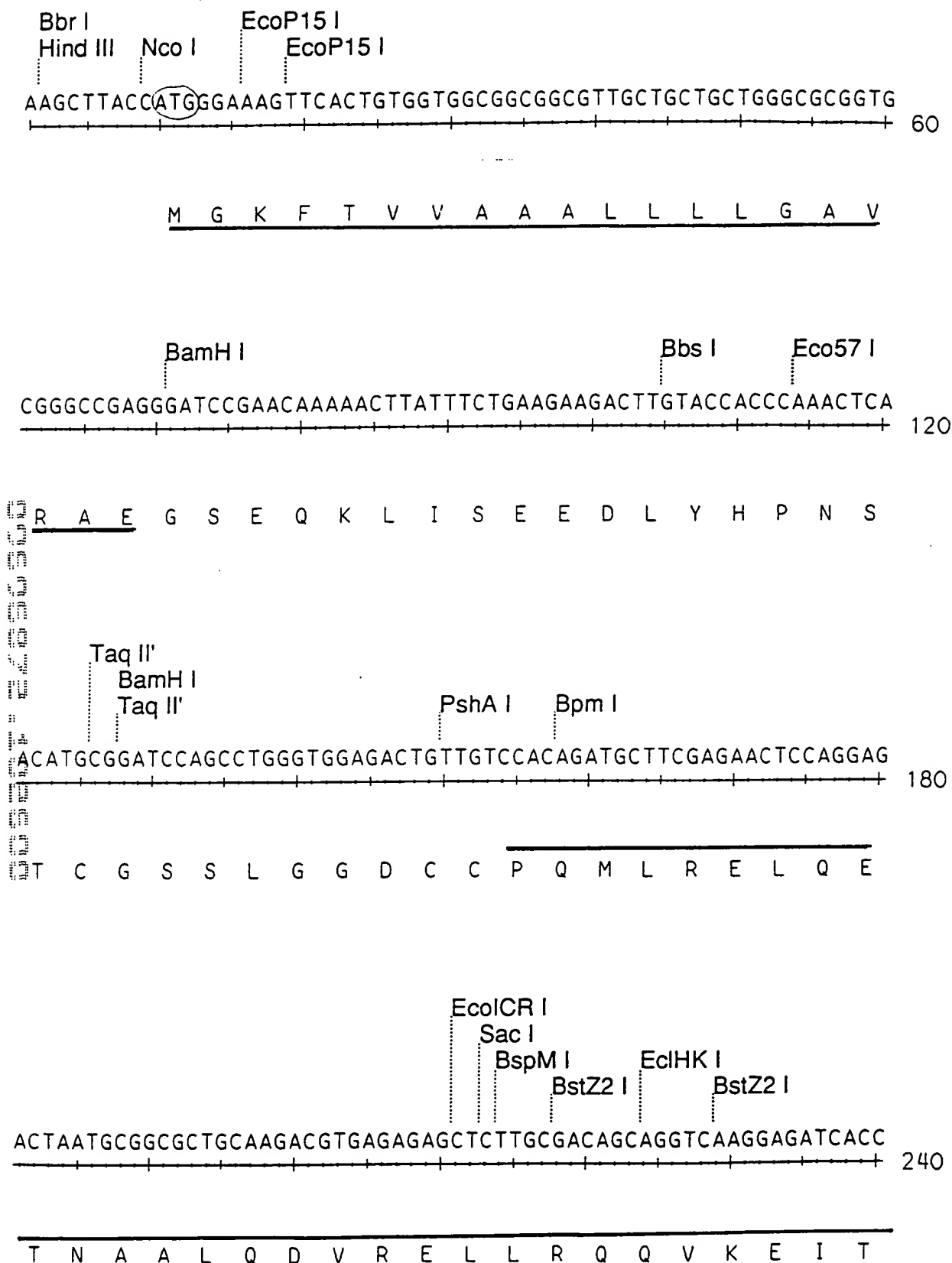


FIGURE 10C.

3188 (sheet 30 of 30)

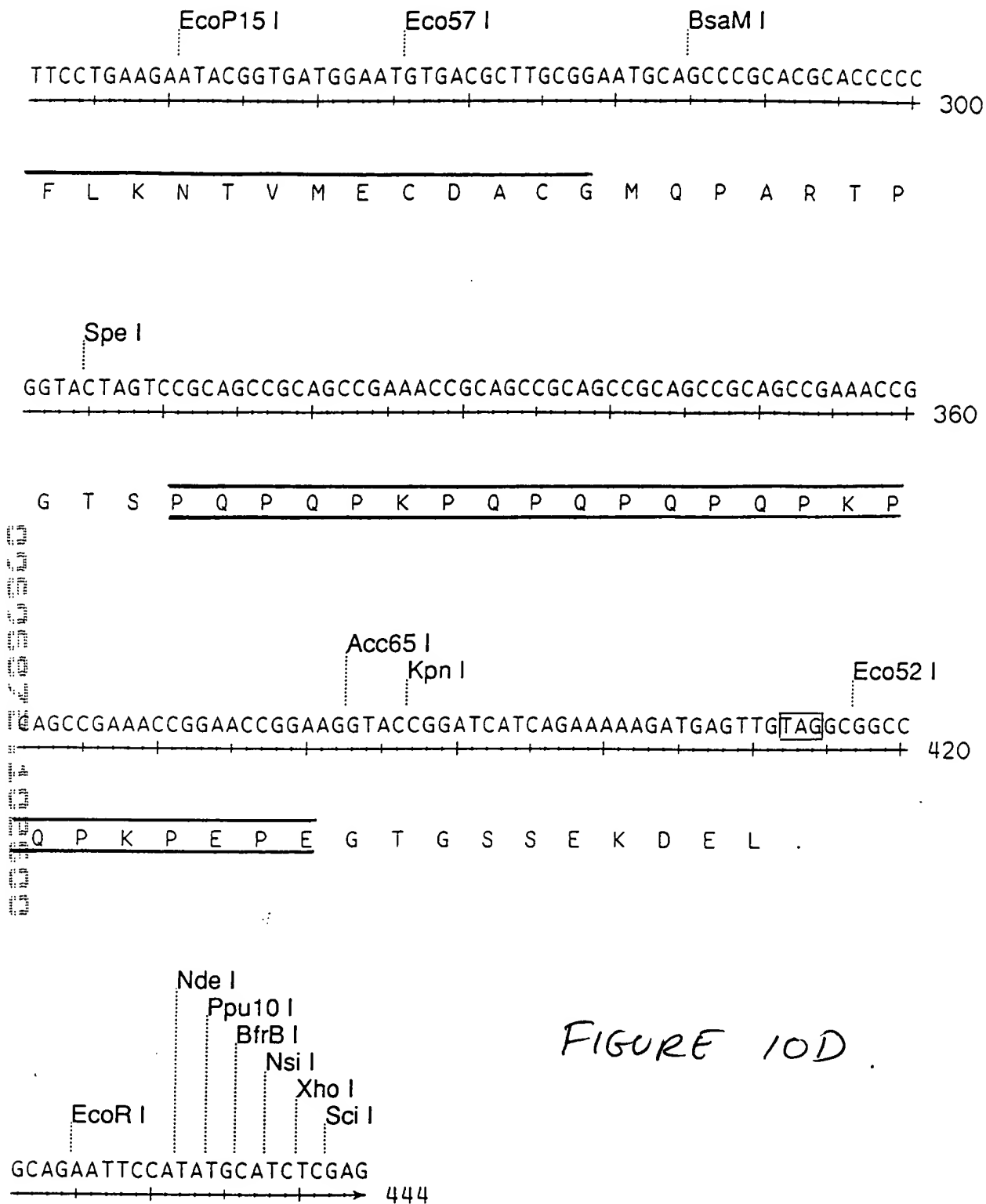


FIGURE 10D .

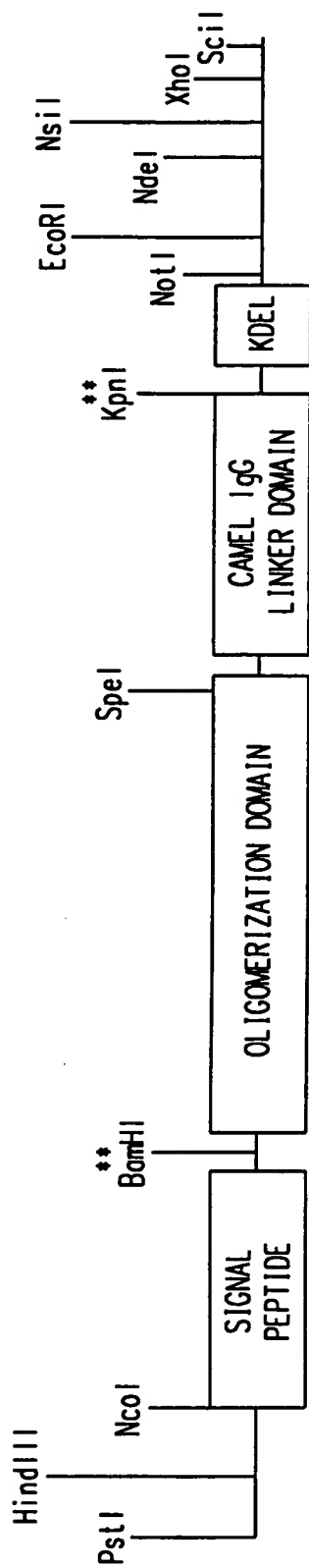


FIG. 1A

SIGNAL CLEAVAGE SITE

MGKFTVVAALLLGAVRAE-GSS-

LGCDLA-PQMLRELQETNAALQDQVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQKPQPQPQPQPQPQPQPQPQPQP-GTCSSE-KDEL

FIG. 1B

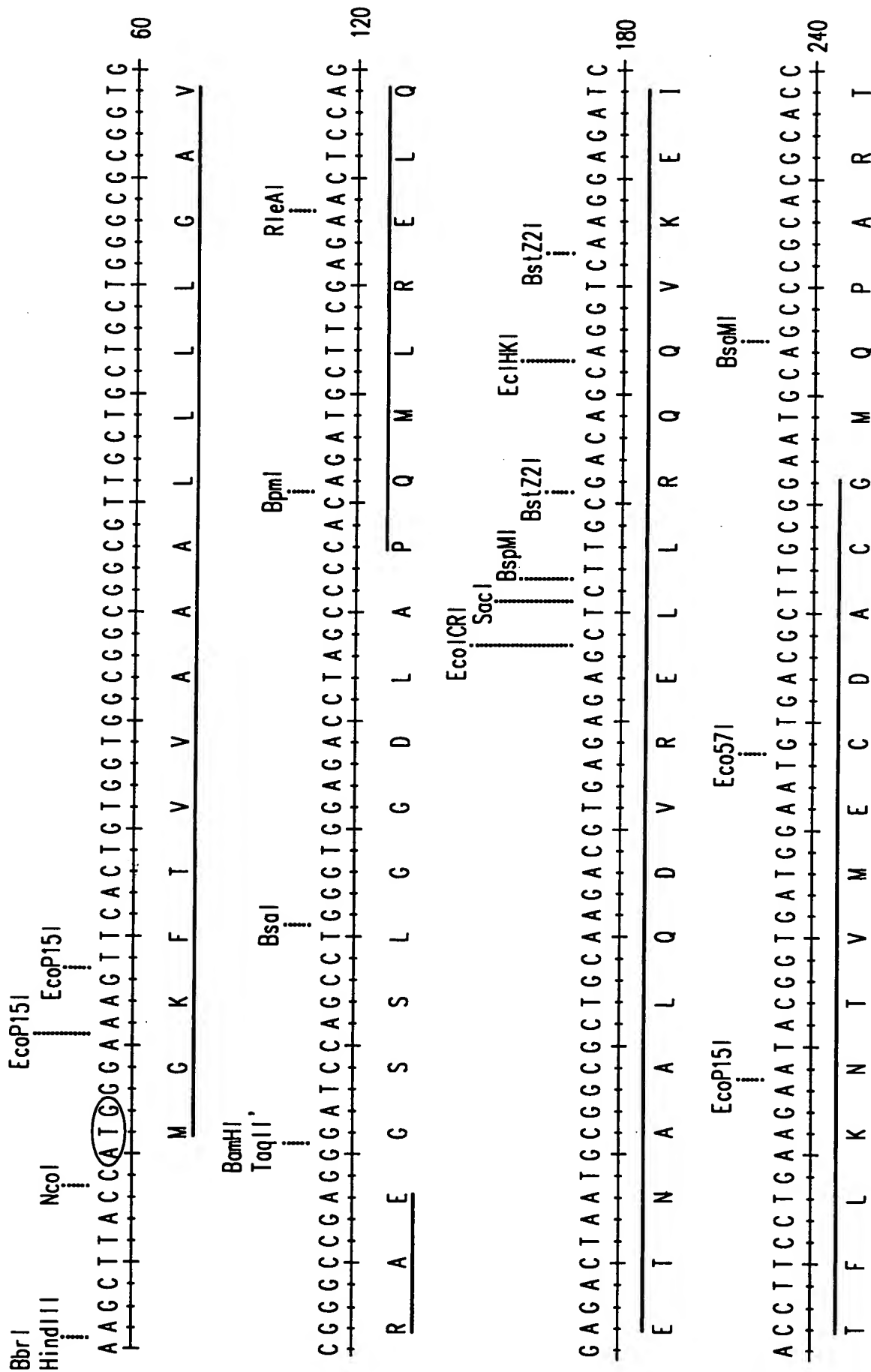


FIG. 1C

SpeI
 C C C G G T A C T A G T C C G G C A G C C G C A A C C C G A G C C G C A G C C G C A G C C G C A A 300

P G T S P Q P Q P K P Q P Q P Q P Q P Q P K

Acc65I KpnI Eco52I
 C C G C A G C C G A A C C G G A A C C G G A G G T A C C G G A T C A G A A A A G A T G A G T G C C G 360

P Q P K P E P E G T G S S E K D E L

NdeI Ppu10I BfrBI NsiI XhoI EcoRI SclI
 G C C G C A G A T T C C A T A T G C A T C T C G A G 387

FIG. 1D

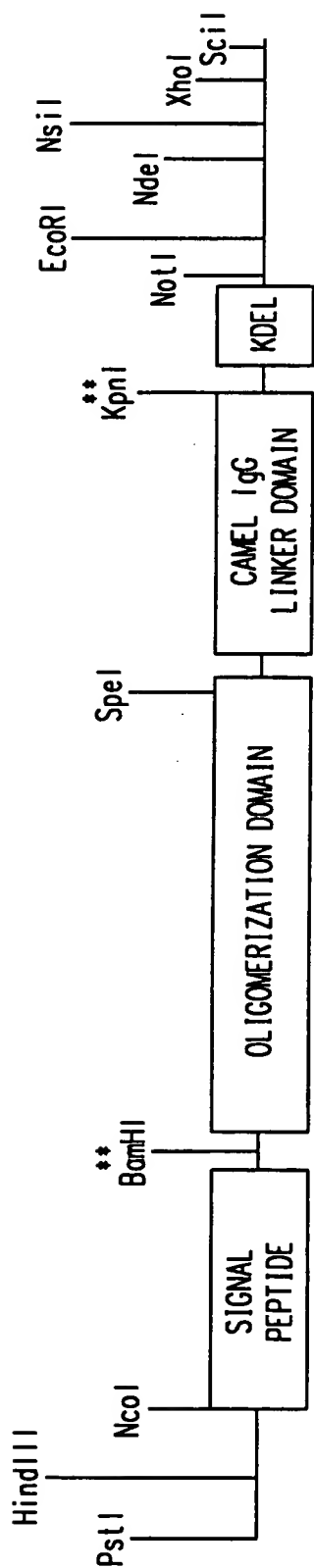


FIG. 2A

SIGNAL CLEAVAGE SITE

M G K F T V A A A L L L G A V R A E - G S S -

L G G D C C - P Q M L R E L Q E T N A A L Q D V R E L L R Q Q V K E I T F L K N T V M E C D A C G - M Q P A R T P G T S -

P Q P Q P K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 2B

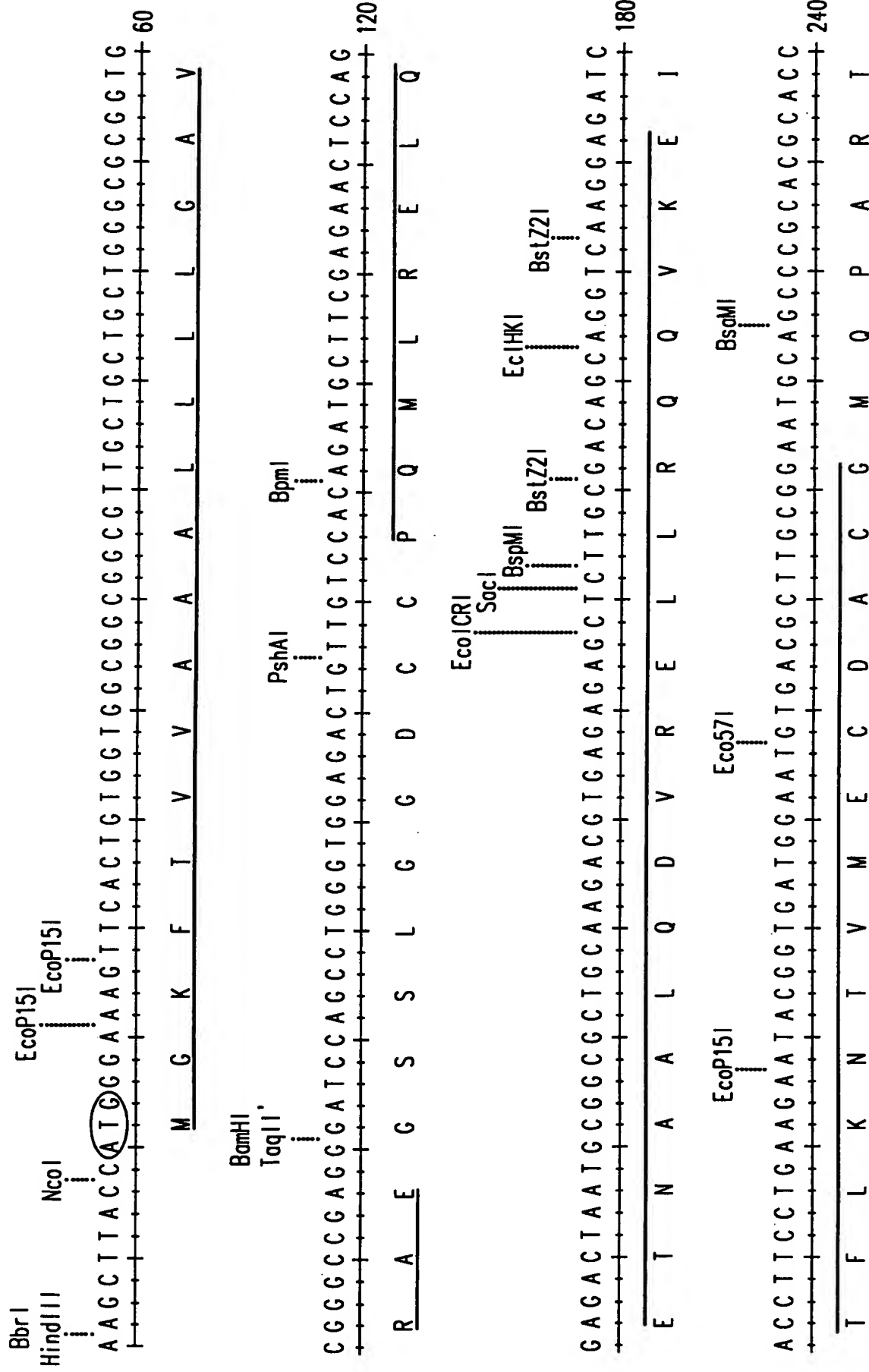
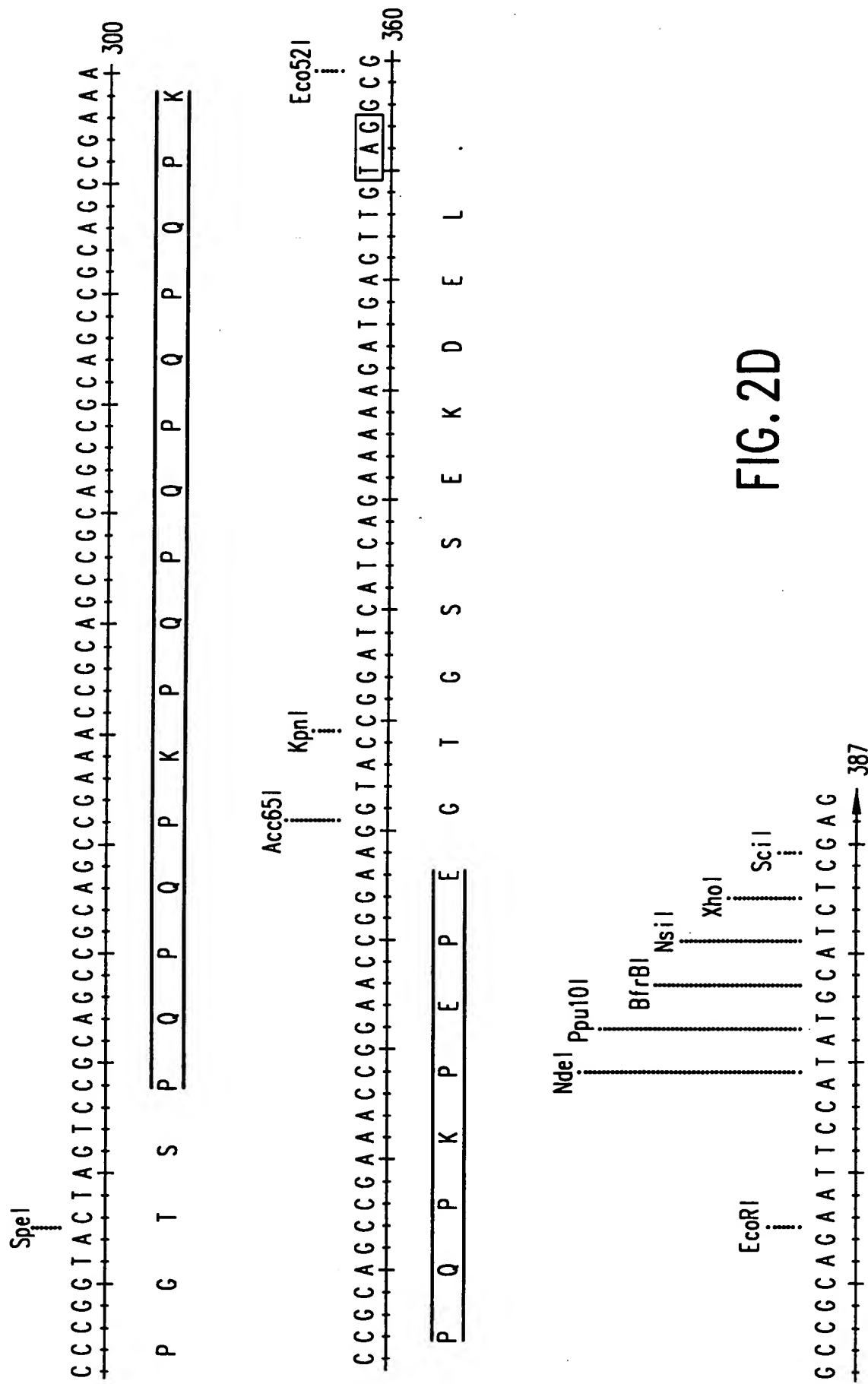


FIG. 2C



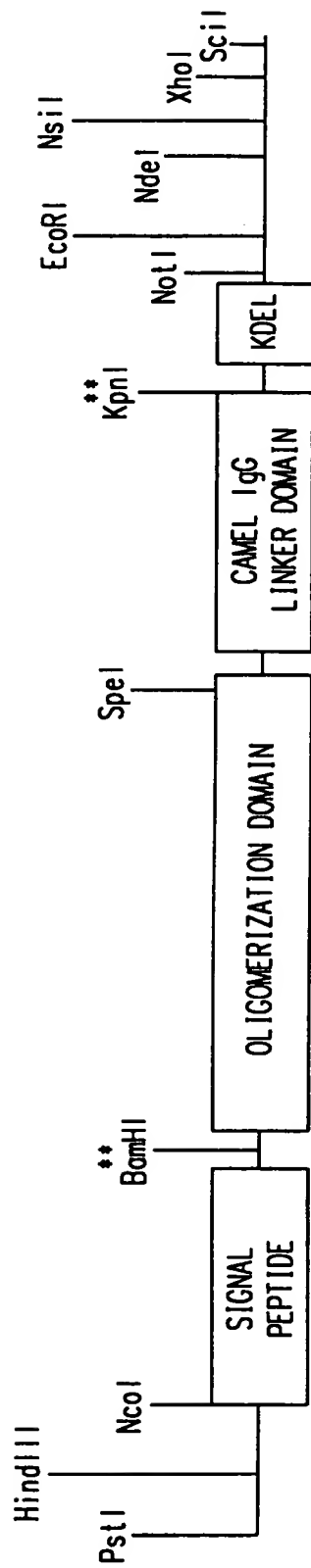


FIG. 3A

SIGNAL CLEAVAGE SITE
 ↓
MCKFTVVAALLLLGAVRAE-GSS-

LGGDCC-KALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-
PQPQKPQPQPQPQPQKPEPE-GTGSSE-KDEL

FIG. 3B

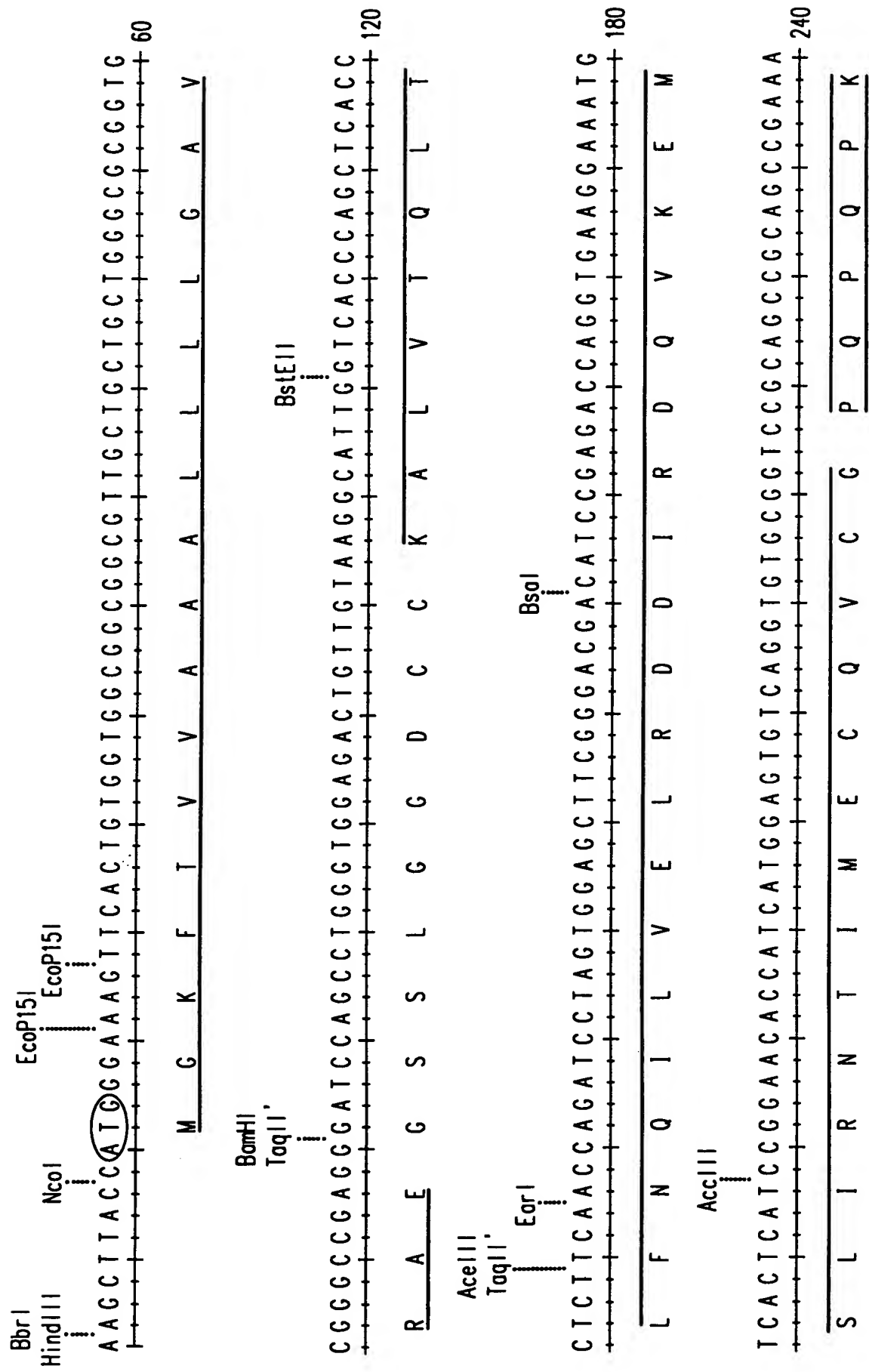


FIG. 3C

CCGCCAGCCCGCAGCCCGCAGCCGGAACCCGGAACCCGGAAGGTACC

Acc65I KpnI

P Q P Q P Q P Q P Q P Q P K P E P E G T

GGATCATCAGAAAGATGAGTTGTTAGCGCGCCCGCAGAAATTCATATGCCATCTCGAG 357
 NdeI Ppu10I BfrBI NsiI XhoI SclI
 Eco52I EcoRI

FIG. 3D

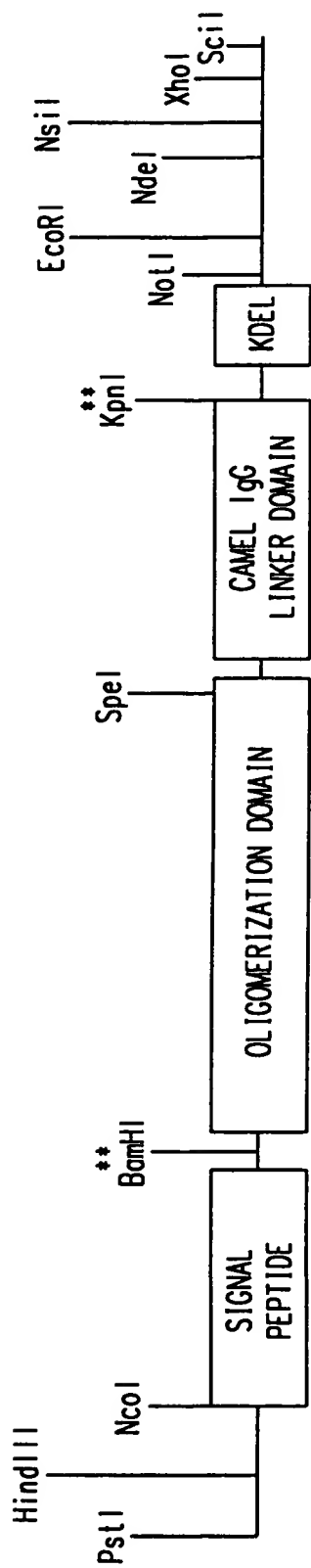


FIG. 4A

SIGNAL CLEAVAGE SITE

M G K F T V A A A L L L G A V R A E - G S S -

L G G D C C - G E Q T K A L V T Q L T L F N Q I L V E L R D D I R D Q V K E M S L I R N T I M E C Q V C G -

P Q P Q K P Q P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 4B

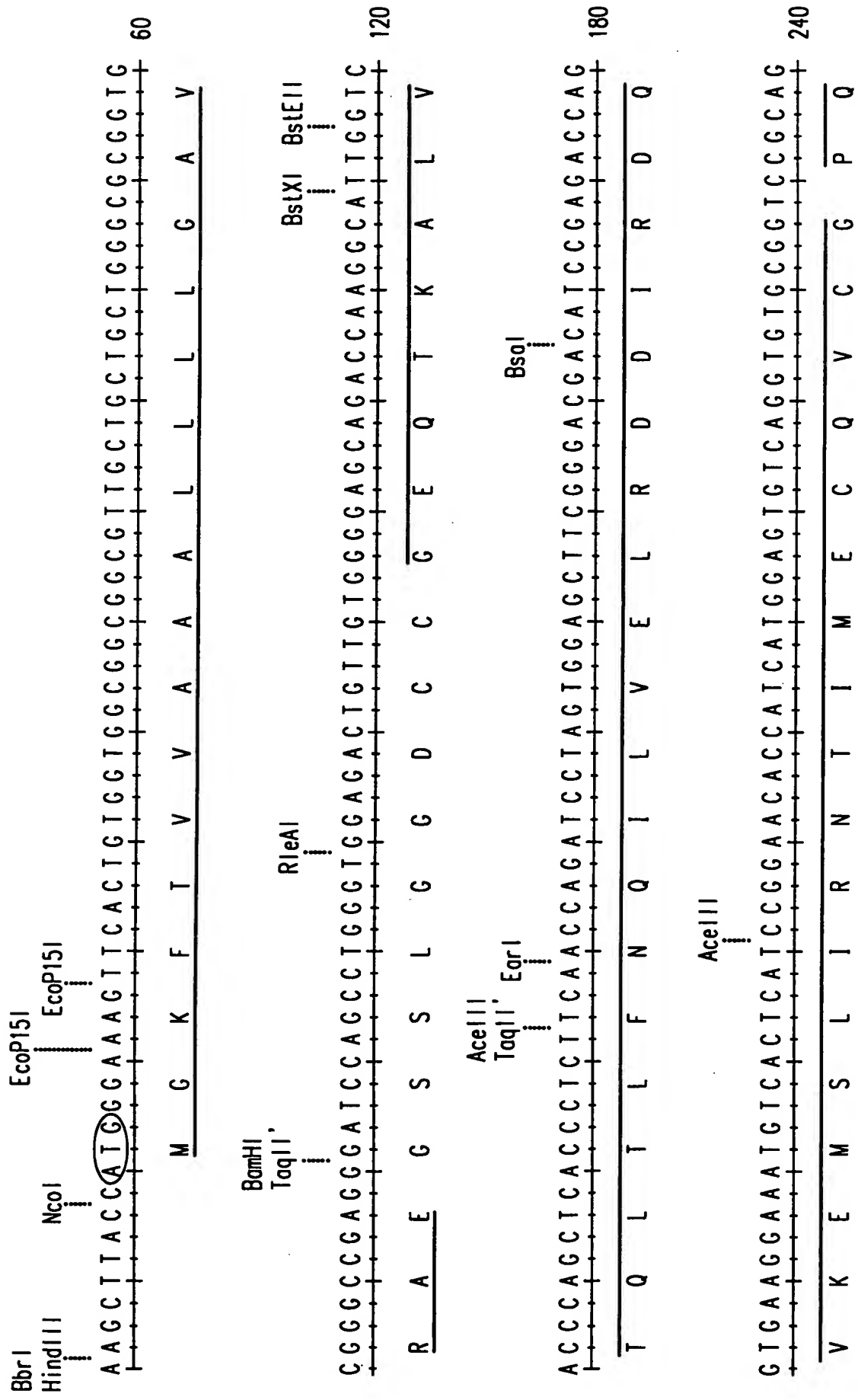


FIG. 4C

CCG CAG CCG GAA ACC GCG CAG CCG CCG CAG CCG CCG GAA ACC GCG CAG CCG GAA ACC CCG GAA

CCG CAG CCG GAA ACC GCG CAG CCG CCG CAG CCG CCG GAA ACC GCG CAG CCG GAA ACC CCG GAA 300

P	Q	P	K	P	Q	P	Q	P	Q	P	Q	P	K	P	Q	P	K	P	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

CCG G A A G G T A C C G G A T C A G A A A A G A T G A G T T G T A G C C G C C C G C A G A A T T C C A T A T G 360

Acc65I KpnI NdeI Ppu10I BfrBI Eco52I EcoRI

P E G T G S S E K D E L

NsiI XhoI SclI
C A T C T C G A G 369

FIG. 4D

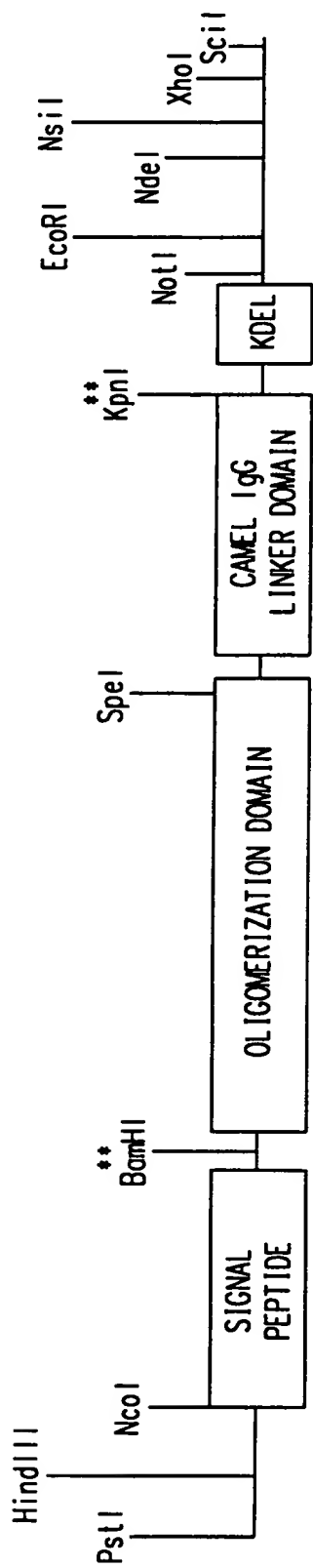


FIG. 5A

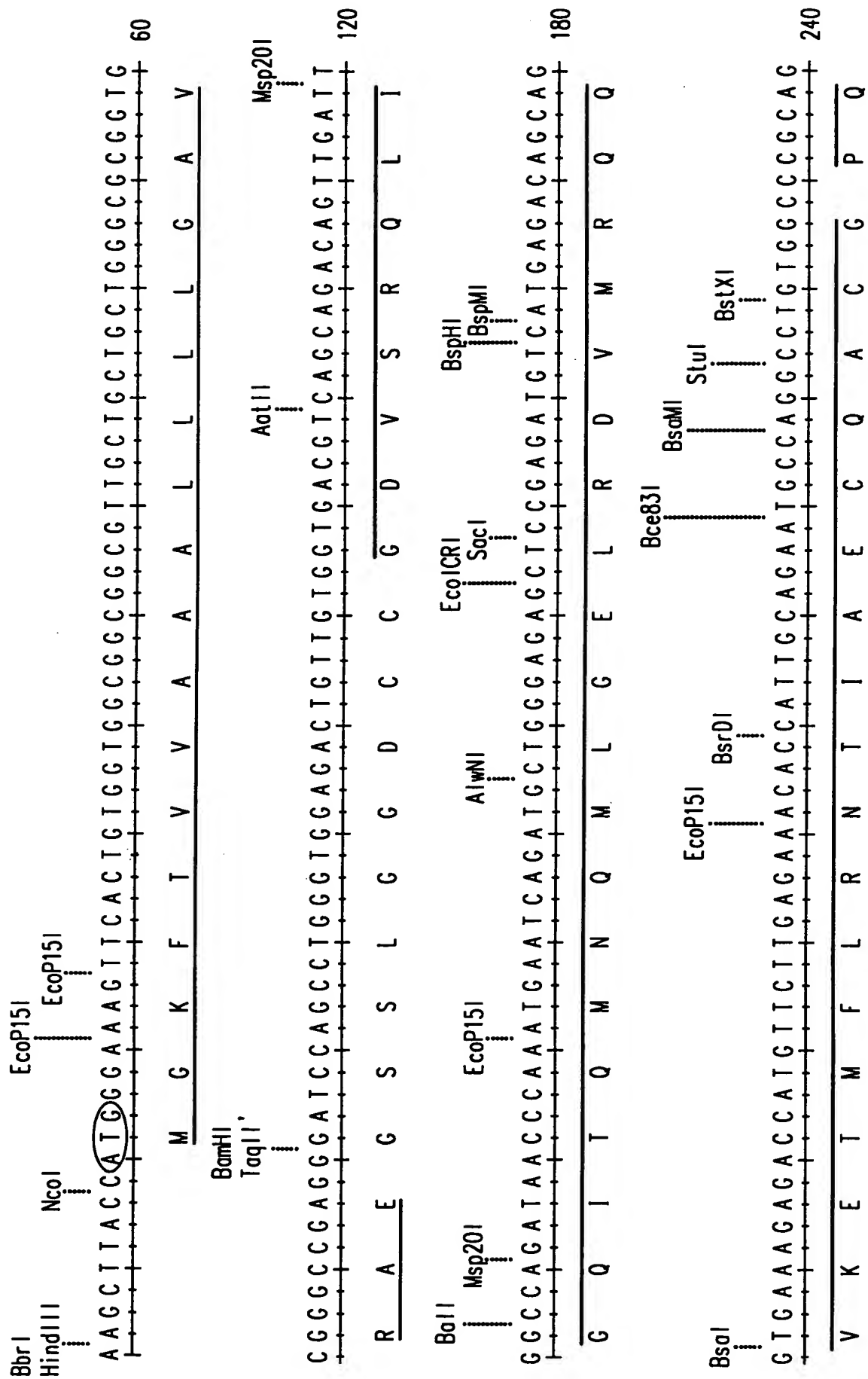
SIGNAL CLEAVAGE SITE

M G K F T V A A A L L L L G A V R A E - G S S -

L G G D C C - G D V S R Q L I G Q I T Q M N Q M L G E L R D V M R Q Q V K E T M F L R N T I A E C Q A C C -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 5B



CCG CAG CCG A A C C G C A G C C G C A G C C G C A G C C G C A A C C G C A G C C G A A C C G G A A 300

P Q P K P Q P Q P Q P Q P Q P Q P K P Q P K P E

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTG[TAG]CCGGCCGCAGAAATTC CATATG 360

Acc65I

KpnI

Eco52I

EcoRI

NdeI

Ppu10I

BfrBI

ATAC

P E G T G S S E K D E L .

NSII
XhoI
SciI
CATCTCGAG 369

FIG. 5D

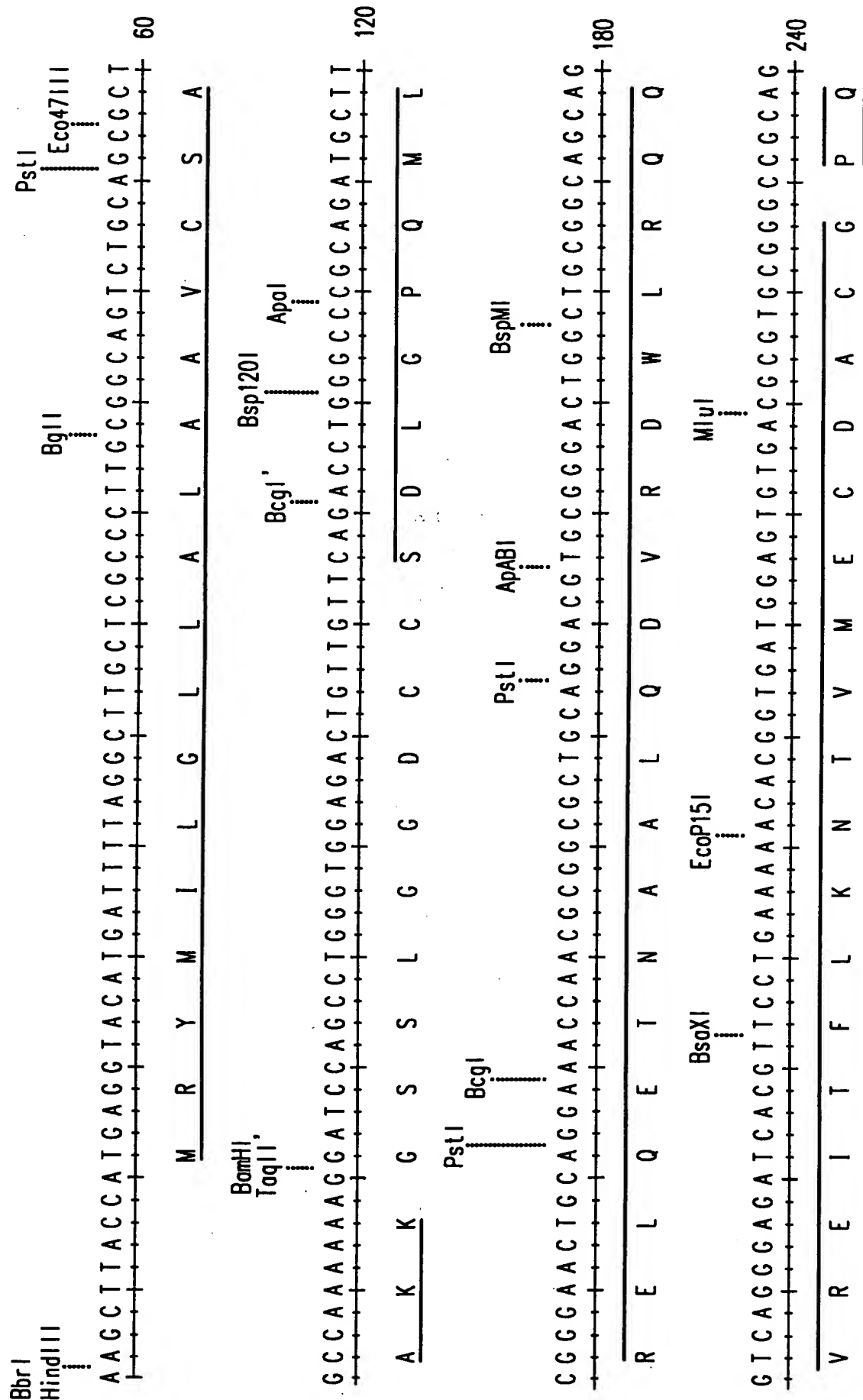


FIG. 6C

P Q P K P Q P Q P Q P Q P Q P Q P Q P Q

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTGTAGCGCGCCGACAGATTCCATATG
 360

Restriction sites (from left to right):
 Acc65I (position 10)
 KpnI (position 20)
 Eco52I (position 100)
 EcoRI (position 110)
 NdeI (position 120)
 Ppu10I (position 130)
 BfrBI (position 140)

P E C T G S S E K D E L

A schematic diagram of a 369 bp DNA fragment. The DNA sequence is represented by a horizontal line with vertical tick marks. The sequence 'CATCTCGAG' is written below the line, with an arrow pointing to the right. Above the line, three restriction sites are indicated: 'NsiI' at the left end, 'XhoI' at a middle position, and 'SclI' at a position further to the right. Vertical lines connect the site names to their corresponding positions on the DNA fragment.

FIG. 6D

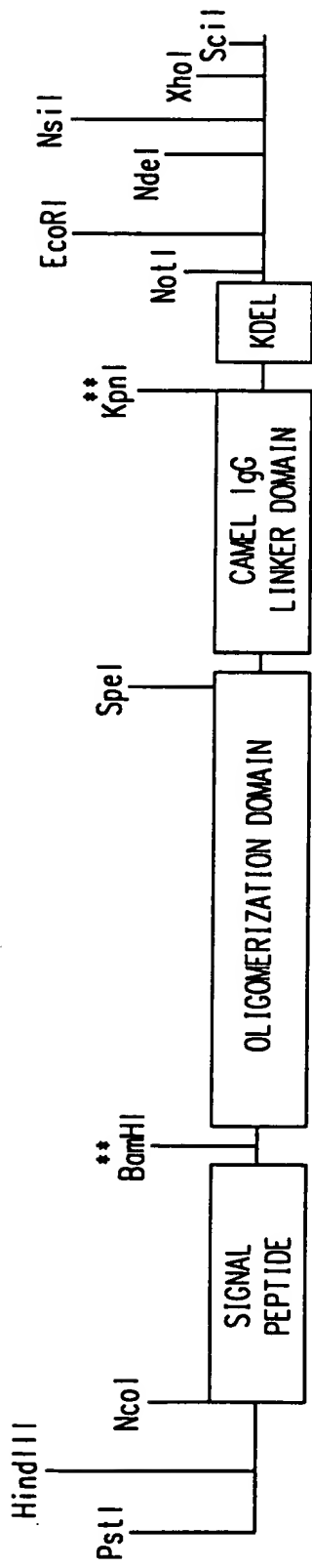


FIG. 7A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - Q K L Q N L F I N F C I L I C L L I C I I V M L L -

P Q P Q K P Q P Q P Q P Q P Q P Q P K P E P E - G T G S S E - K D E L

• RESIDUES CRITICAL FOR PENTAMER FORMATION

FIG. 7B

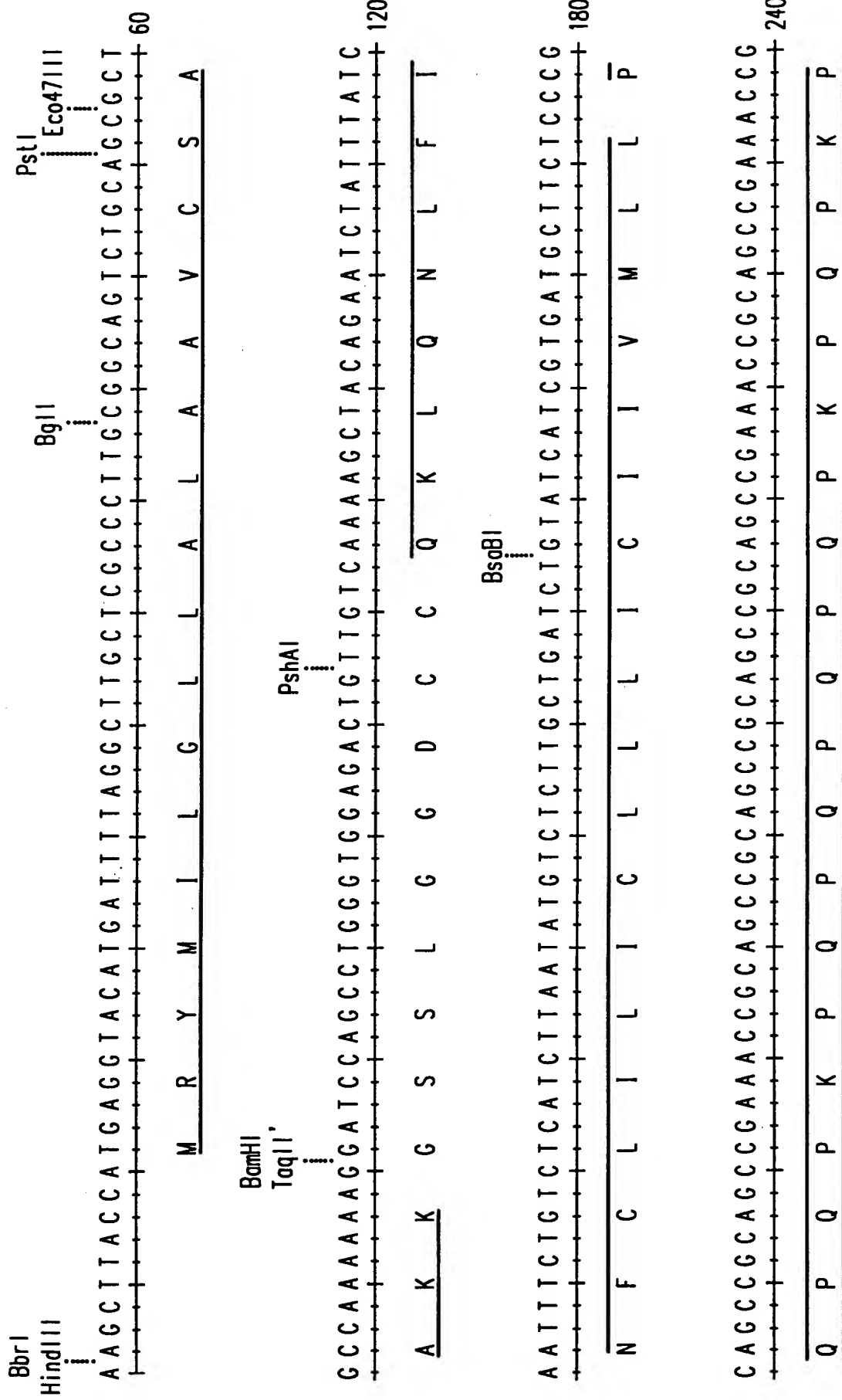


FIG. 7C

Acç65I
 KpnI
 Eco52I
 EcoRI
 NdeI
 300
 GAACCGGAAGGTACCCGGATCATCAGAAAAGATGAGTTGTAGCGGCCGCAGATTCCAT
 E P E G T G S S E K D E L

The diagram shows a 312 bp DNA fragment with the sequence ATGCATCTCGAG. Restriction sites are indicated by vertical lines above the sequence: Ppu10I (at the start), Bfr8I (at position 10), NsiI (at position 20), XhoI (at position 30), and SclI (at position 40). The fragment size 312 is indicated at the right end with an arrow.

FIG. 7D

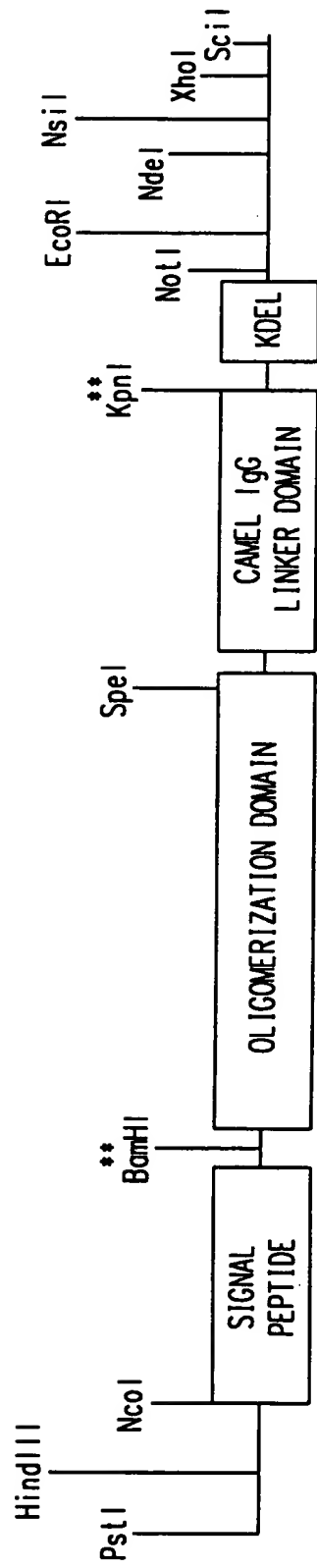


FIG. 8A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - G E Q T K A L V T Q L T L F N Q I L V E L R D D I R D Q V K E M S L I R N T I M E C Q V C G -

P Q P Q K P Q P Q P Q P Q P K P Q K P E P E - G T G S S E - K D E L

FIG. 8B

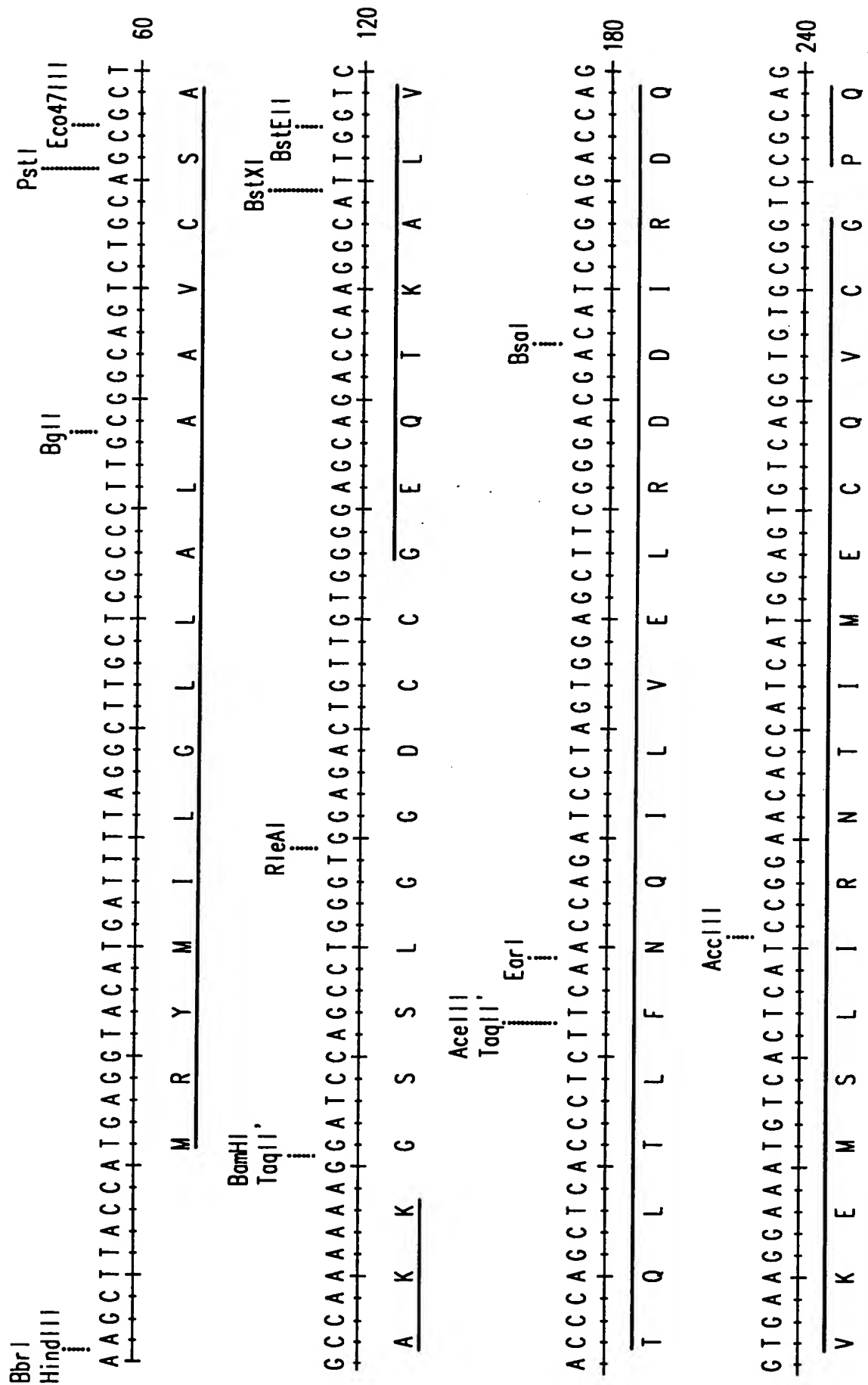


FIG. 8C

P	Q	P	K	P	Q	P	Q	P	Q	P	Q	P	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---

Acc65I
 KpnI
 Eco52I
 EcoRI
 Ppu10I
 NdeI
 BfrBI
 360

CCGGAAGGTACCGGATCATCAGAAAGAATGAGTTGTAGCCGCCAGCAATTCATATG

P E C T C S S E K D E L

FIG. 8D

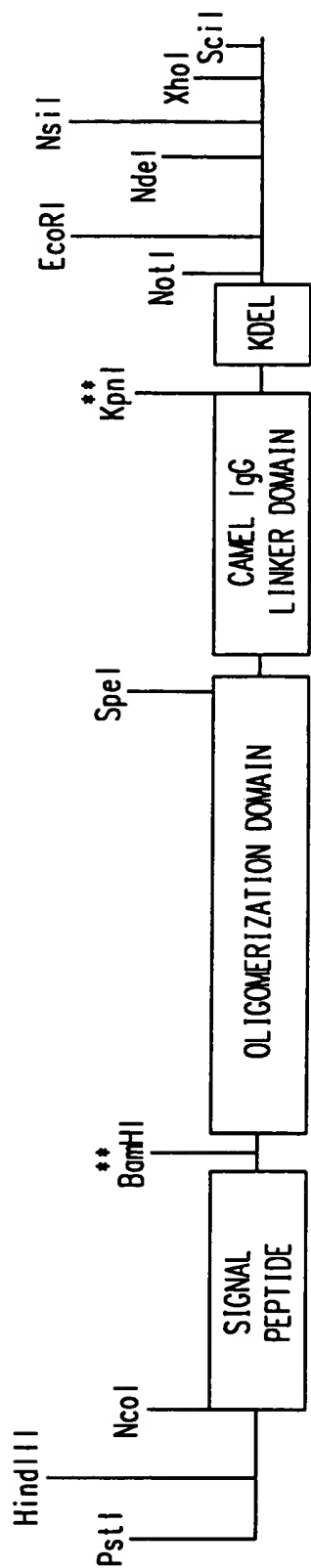


FIG. 9A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - G D F N R Q F L G Q M T Q L N Q L L G E V K D L L R Q Q V K E T S F L R N T I A E C Q A C G -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 9B

CCGCCAGCCGAAACCGCAGCCGGCAGCCGGCAGCCGGAACCGCAACCGGA
300

P Q P K P Q P Q P Q P Q P Q P Q P Q P Q

CCGGAAGGTACCGGATCATCAGAAAGAATGAGTTGTAGCGCGCCGACAGATTCCATATC

Acc65I KpnI Eco52I EcoRI NdeI Ppu10I BfrBI

360

P E T R U S S E K D E L

FIG. 9D

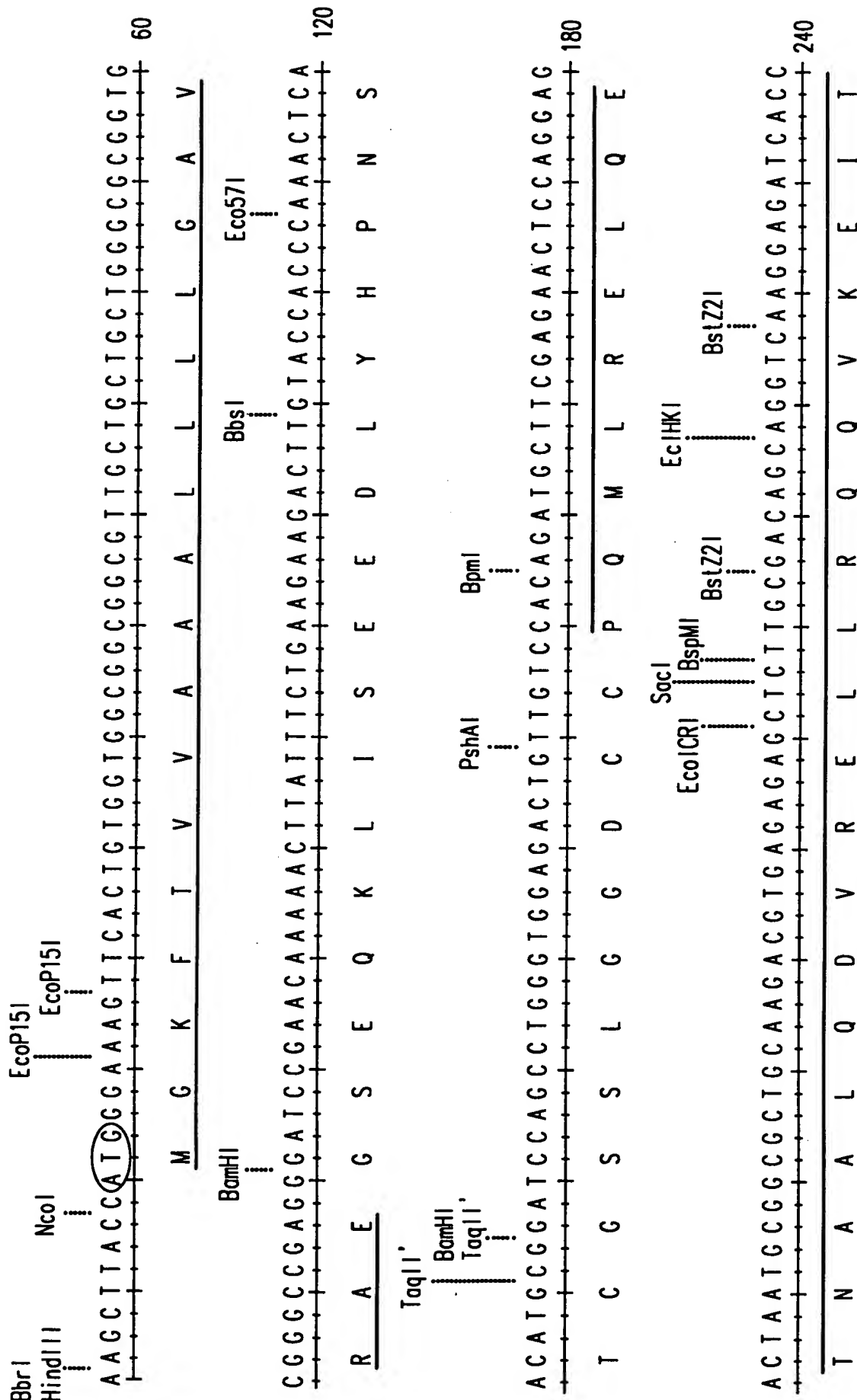


FIG.10C

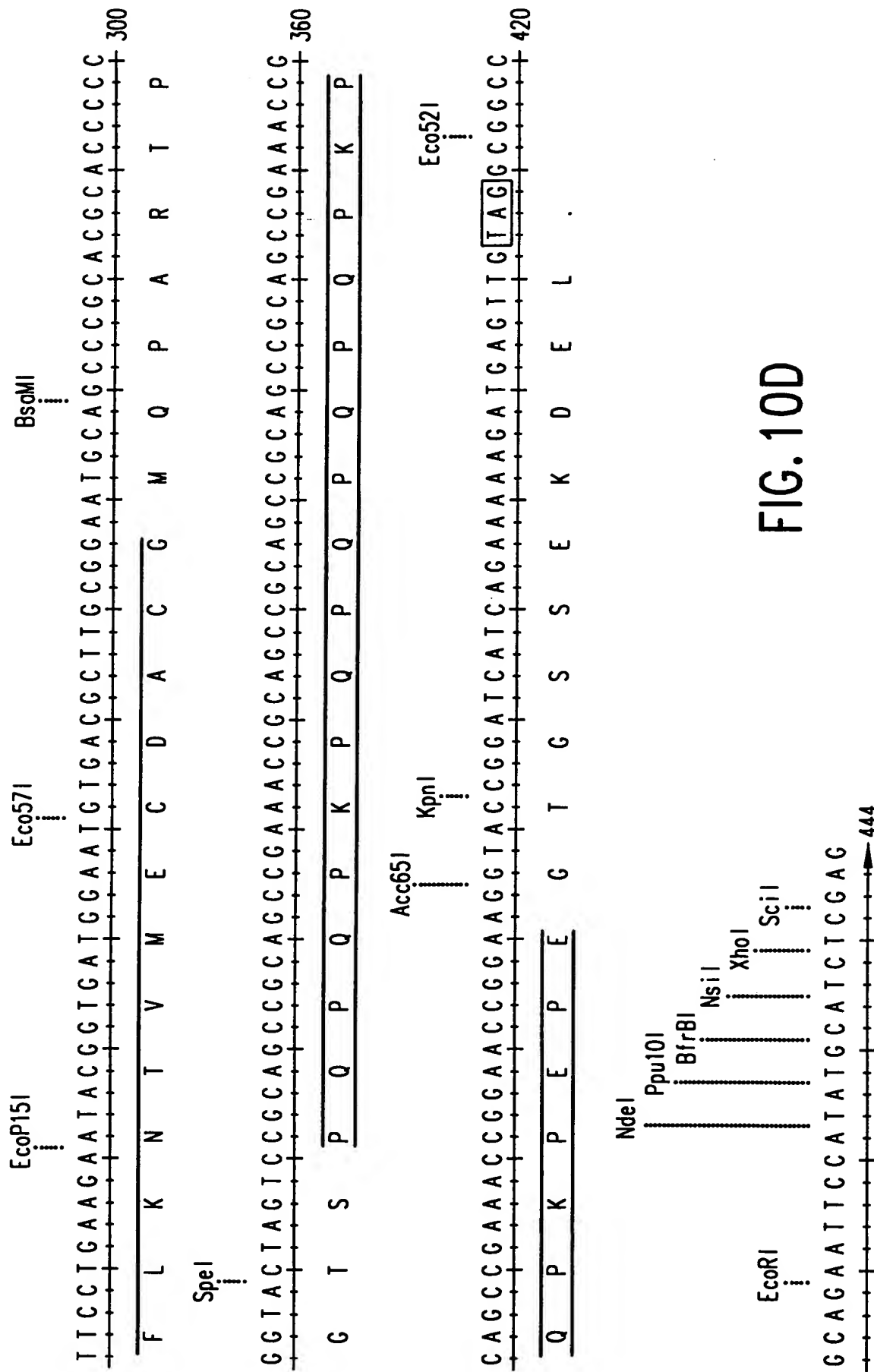


FIG. 10D